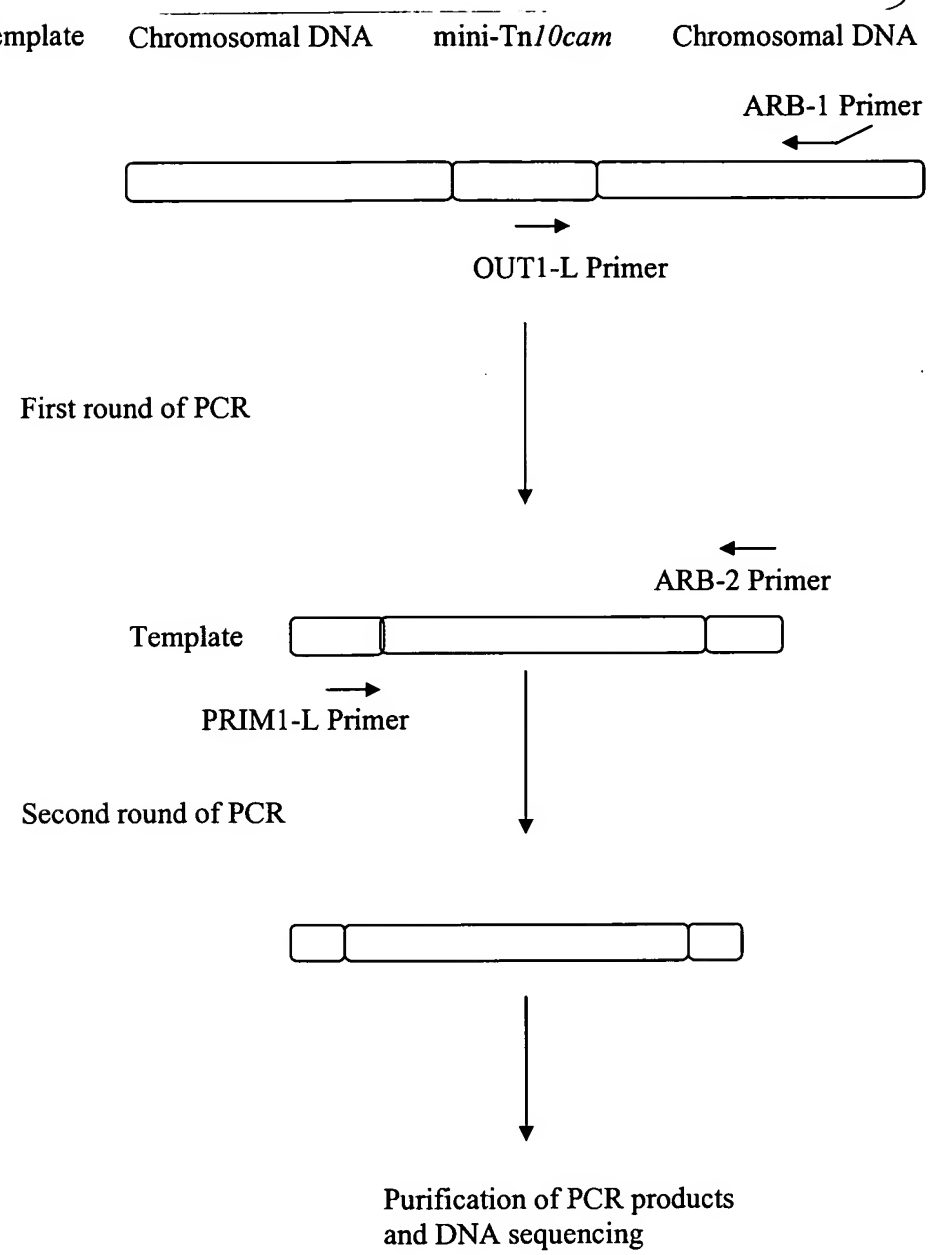
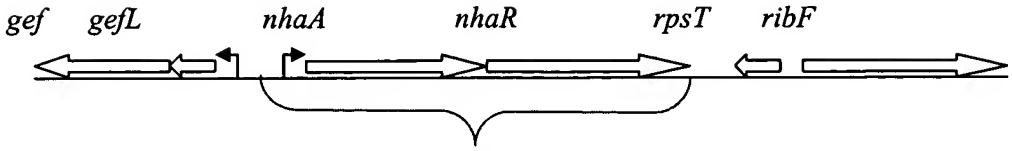
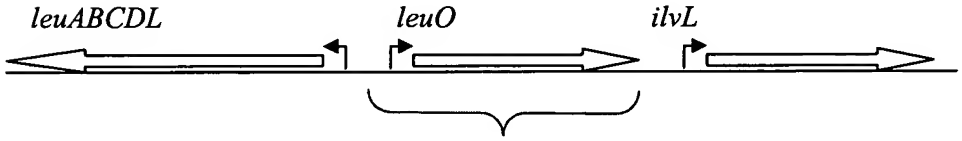


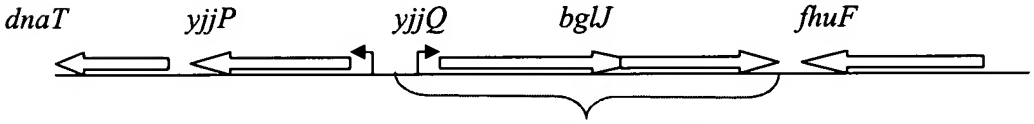
Figure 1



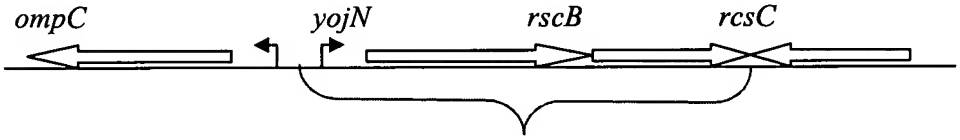
Genome included in cloning *hnaR*



Genome included in cloning *leuO*



Genome included in cloning *yjjQ*



Genome included in cloning *yojN*

Open reading frames or coding regions (⇨);
predicted promoters (↱);
cloned regions (⤿)

Figure 2

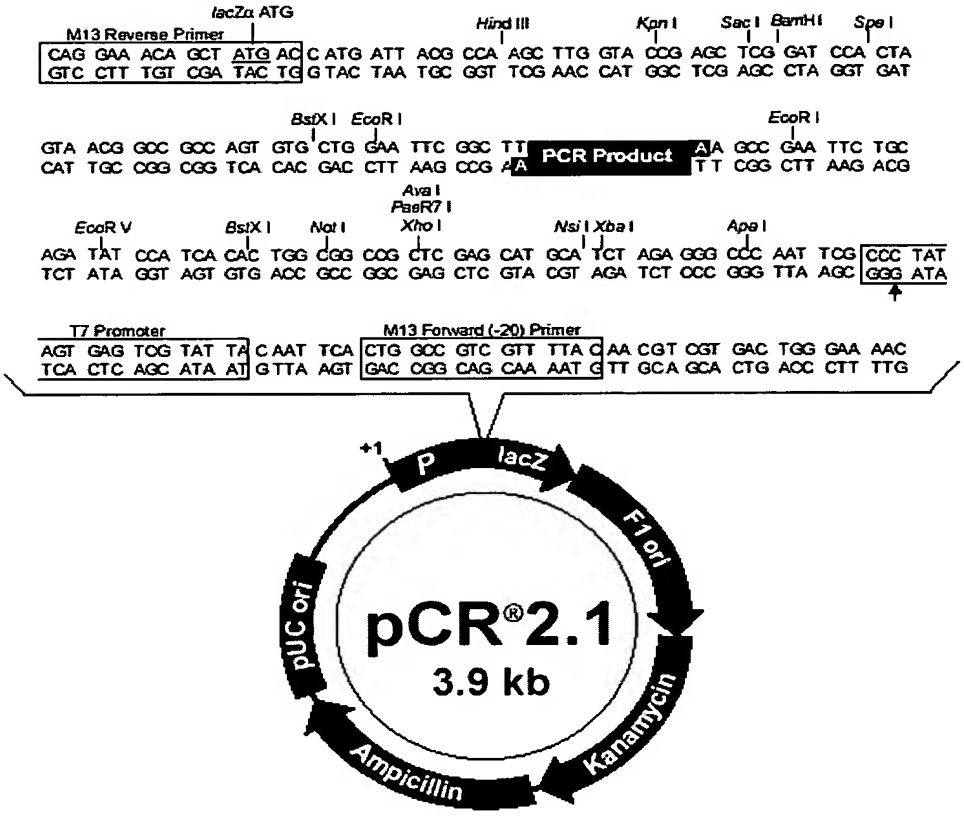

lacZα ATG
M13 Reverse Primer
Hind III
Kpn I
Sac I
BamH I
Spe I
CAG GAA ACA GCT ATG AC C ATG ATT ACG CCA AGC TTG GTA CCG AGC TCG GAT CCA CTA
GTC CTT TGT CGA TAC TG GTAC TAA TGC GGT TCG AAC CAT GGC TCG AGC CTA GGT GAT
BstX I
EcoR I
EcoR I
GTA ACG GCC GCC AGT GTG CTG GAA TTC GGC TT
CAT TGC CGG CGG TCA CAC GAC CTT AAG CCG AA
PCR Product
TA GCC GAA TTC TGC
TT CGG CTT AAG ACG
Ava I
PaeR7 I
EcoR V
BstX I
Not I
Xho I
Nsi I
Xba I
Apa I
AGA TAT CCA TCA CAC TGG CGG CCG CTC GAG CAT GCA TCT AGA GGG CCC AAT TCG CCC TAT
TCT ATA GGT AGT GTG ACC GCC GGC GAG CTC GTA CGT AGA TCT CCC GGG TTA AGC GGG ATA
T7 Promoter
M13 Forward (-20) Primer
AGT GAG TCG TAT TA C AAT TCA CTG GCC GTC GTT TTA C AA CGT CGT GAC TGG GAA AAC
TCA CTC AGC ATA AT G TTA AGT GAC CGG CAG CAA AAT G TT GCA GCA CTG ACC CTT TTG
+1
P
lacZ
F1 ori
pUC ori
pCR®2.1
3.9 kb
Ampicillin
Kanamycin

Figure 3

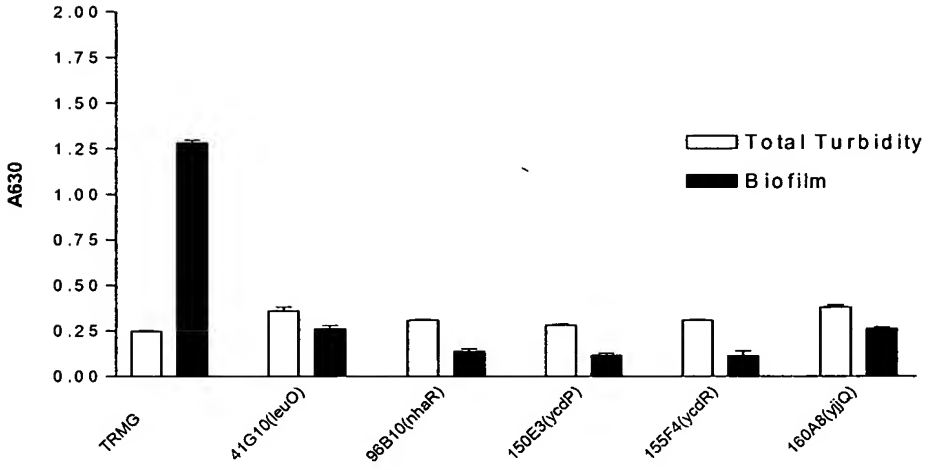


Figure 4A

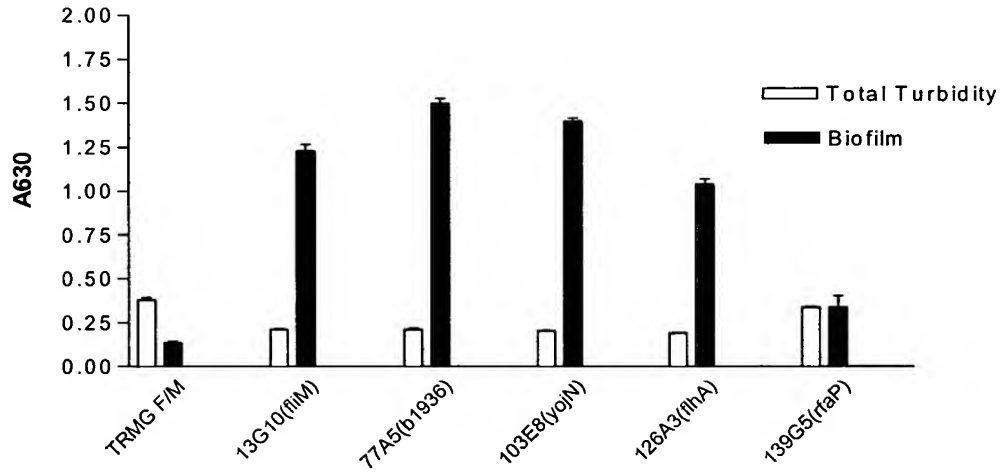


Figure 4b

Figure 5-1

1B10 (10X)
fliD gene - flagella biosynthesis; filament capping protein, enables filament assembly

Transposon Tn10 Accession # AY528506
Nucleotide Accession # AE000285
Protein Accession # AAC74991

AAAAACGGTTACCGGATCCGGGATCATATGACAAGATGTGTATCCACCTTAACTTAATGATTTTTACCAAAATCATTAGGGG
ATTCATCAG
GGTCAGGTCTGGATTTAAGTTCCATCCTTGATAGCCTCACCGCCGCGCAAAAAGC
GACGCTAACCCCCATTTCAAATCAGCAATCGTCGTTTACCGCTAAACTTAGCGCC
TACGGTACGCTGAAAAGCGCGCTGACGACTTTCCAGACCGCCAATACTGCATTGT
CTAAAGCCGATCTTTTTTCCGCCACCAGCACCACCAGCAGCACCACCGCGTTC

Figure 5-2

12E12-6 (7x)
rfaG gene – enzyme, macromolecule metabolism; glucosyltransferase I, LPS core biosynthesis

Transposon Tn10 Accession # AY528506
Nucleotide Accession # S75736
Protein Accession # AAD43826

AAAAACGGTTACCGGATCCGG
GATCATATGACAAGATGTGTATCCACCTTAACTTAATGATTTTTACCAAAATCATTAGGGGATTCATCAG
AGTTAAGTCCCATACCAACCATGGACGCAATGCAGAATATTATGCCTGGGTACAAAATCATCTCAA
AGAGCATCCCGCAGATCGCGTTGTTGGGTTTAATAAGATGCCTGGCCTGGATGTTTATTTTGCCGC
TGATGTTTGTTACGCCGAGAAAGTTGCGCAAGAAAAAGGTTTTTTATATCGTTTAACATCACGATA
TCCNCNNNNNNNGTACTAGTCGACGCGGGGCCAANNN

Figure 5-3

13G10-4 (11X)
fliM gene - Structural component; surface structures/flagellar biosysnthesis, component of motor switch/energizing

Transposon Tn10 Accession # AY528506
Nucleotide Accession # AE000286
Protein Accession # AAC75012

NAAAAACCCGCCGGACATCCCGGATCCGG
GATCATATGACAAGATGTGTATCCACCTTAACTTAATGATTTTTACCAAAATCATTAGGGGATTCATCAG
TGTTCAACCTGCTGCGTCGTAGCCCGGATATATCCNNCNNCNCNGNACTAGTCGACGCGTGGCCA

Figure 5-4

14C10-4 (10X)
flgE gene – structural component; surface structures/ flagellar biosynthesis, hook protein

Transposon Tn10 Accession # AY528506
Nucleotide Accession # AE000208
Protein Accession # AAC74160

AACGGNCCGATCCGG
GATCATATGACAAGATGTGTATCCACCTTAACTTAATGATTTTTACCAAAATCATTAGGGGATTCATCAG
AGATCANCCTGAATTCCAGTGATCCGCTTCCTACTGTTACGCCATTCANNGCCNGCAATGCGGNTANCTNTN
ACAAANAAGGTTNNGTGACTGTTTTCCACAGTCATGGTAATGCTCATGACATGAGCGTCTACTTTGTGNACC
CGGGGATAATAACTGGCAGGTCTACACCCAGGATAGCAGTGATCCAAACAGCATTGCGAAGACAGCG

Figure 5-5

36E2-5 (3X)
yhjH gene (complement) - orf; unknown function ; hypothetical protein

Transposon Tn10 Accession # AY528506
Nucleotide Accession # NC_004431
Protein Accession # NP_417982

AAACGGTTACCGGATCCGG
GATCATATGACAAGATGTGTATCCACCTTAACTTAATGATTTTTACCAAAATCATTAGGGGATTCATCAG
TGCTTACACCTGGCAGCCGATCTATCAAACATGCGGGCGGTTAATGGCCGTGGAGCTATTAACGGT
GGTCACGCATCCCTTGAACCCTTCGCAACGCCTGCCGCCGGATCGCTATTTTACTGAAATCACCGT
CAGCCATCGGATGGAGGTTGTGAAAGAGCAGATTGATTTGCTGGCGCAAAAAGCCGACTTCTTTAT
AGAGCACGGCCTGCTGGCATCGGTCAATAT

Figure 5-6

38G7-2 (11X)
fliM gene - Structural component; surface structures/flagellar biosysnthesis, component of motor switch/energizing

Transposon Tn10 Accession # AY528506
Nucleotide Accession # AE000286
Protein Accession # AAC75012

AAACGGTTACCGGATCCGG
GATCATATGACAAGATGTGTATCCACCTTAACTTAATGATTTTTACCAAAATCATTAGGGGATTCATCAG
CTTCAAGCGCCAGTTTCAACATGCGGTTGATGACGCGCTGTTCGGTATGGGTAAACTCGCGACCTT
CCACTTTGGTCGGGAAGCGTCCATCGCCGCCAAACAGGTTATCCACGGCGATAAACACCAGACTC
GGTGAGAACACCACCAGCCCAGTGCCGCGCAGCGGTTTCAGATGGATAAGGTTCAGGTTGGTCGG
CACCGGCAGGTTGCGGGCAAATTCATGGTACGGCTGAATGCGGATGGCCCCGACGGTTATATCCN
GNCNNNNNGTACTAGTCGACG

Figure 5-7

39C9-2 (3X)
rep gene - enzyme; DNA replication, repair restriction/modification; product - rep helicase, a single-stranded DNA dependent ATPase

Transposon Tn10 Accession # AY528506
Nucleotide Accession # AE000454
Protein Accession # AAC76783

AAACGGTTACCGGATCCGGGATCATATGACAAGATGTGTATCCACCTTAACTTAATGATTTTTACCAAAATCATTAGGGGATT
CATCAG
TATCCAGCCCCAACGTATGGAAAGTGGAGATCATCAGCCCACGCGCCTCTTTGCGCCCCAGCGTCT
GCCCTACACGCTCTTTCATCTCGCGCGCTGCTTTATTAGTAAAGGTCACCGCCGCAATGTGCCGCG
CCTGATAACCGCAACCGCGGATCAGATGGGCGATTTTATTGGTGATAACACGAGTTTTACCGGAAC
CCGCGCCCGCCAGCACCAGGCAGGGGCCGGTAACGAATTCGACAGCTTGTTGTTGGCCGGGGTTT
AGACGCATAGGTGTATTGCTCA

Figure 5-8

42G6-4 (12X)
fliP gene – putative structure; surface structures/ flagallar biosynthesis

Transposon Tn10 Accession # AY528506
Nucleotide Accession # AE000287
Protein Accession # AAC75015

CGGNCCGGATCCGG
GATCATATGACAAGATGTGTATCCACCTTAACTTAATGATTTTTACCAAAATCATTAGGGGATTCATCAG
TGGTACGCATCTACATAAATTTTGTCGATCACCGGTGACATAATAAAAAAGGTCAAAAACAGTGC
CAGCCCCAGCAATACCTGGTTAGGTGGCGCGCGGAGGGTGTTCCCAGCGCGTTACGCAATAAACC
AAAAACAATGATGATGCGGGTGAAACTGGTCATCATCAGTAAAATTGCCGGAATAAACGTCAACG
AGGTGATGAACACCAGCGTCTGCACCGGGAGC

Figure 5-9

43B10-3 (11X)
fliG gene – Structural component; surface structure, flagella motor component

Transposon Tn10 Accession # AY528506
Nucleotide Accession # AE000286
Protein Accession # AAC75006

NNCNNAACANACGGNNCCGGCCNG
GATCATATGACAAGATGTGTATCCACCTTAACTTAATGATTTTTACCAAAATCATTAGGGGATTCATCAG
CGGCGAGCTGGCGCAGAAAATCATCGACGAGATGTTCCTGTTCGAGAATCTGGTGGATNTCGCCAATCGCN
GTACTAGTCGACGNGTGGCCAAANTGGATTCCNAATCGCTGNTGATCGCGCTGAAAGGAGCCGAGCNGTC
ACTGTGCNAGAANTTCTTGCNCNATATGTCGCNNCGTGCCGCCNATATCCCNCNCCNACCGTACCCCTNGN
ACGNNNNACCNGNACCCCNNTNCGGNCAAGNATGNNANNANCCNGATANANCAGNNCANTNCTNNGATN
CACNNNATANNANNGNCGCCNAC

Figure 5-10

43F5-2 (2.5X)
wecB gene - enzyme; Central intermediary metabolism; sugar-nucleotide synthesis, product - UDP -N-acetyl glucosamine-2-epimerase

Transposon Tn10 Accession # AY528506
Nucleotide Accession # AE000455
Protein Accession # AAC76791

AAACGGTTACCGGATCCGG
GATCATATGACAAGATGTGTATCCACCTTAACTTAATGATTTTTACCAAAATCATTAGGGGATTCATCAG
GGTCAGGCATGCTCTCGCATTCTGGAAGCGTTAAAAAATAATCGGATATCACTATGAGTTTTGCGA
CCATTTCTGTTATCGGACTGGGTTATATCGGGCTGCCAACNGCTACNCGACNCGCGCCNCGGCAAA
AACAGGTAATTGGTGTCGATATCAACCAACATGCGGTTGATACCATCAATCGTGGCCAAATCCATA
TCCCCCCCCCCCGTACTAGTCGACG

Figure 5-11

45C8-4 (4X)
frdA gene – enzyme; energy metabolism, carbon: anaerobic respiration; product is fumarate reductase, anaerobic flavoprotein subunit

Transposon Tn10 Accession # AY528506
Nucleotide Accession # AE000487
Protein Accession # AAC77114
CGGNCCGGATCCGG
GATCATATGACAAGATGTGTATCCACCTTAACTTAATGATTTTTACCAAAATCATTAGGGGATTCATCAG
TGCCGCGCACGGCAAATCCGAATGCAAAAATCGCACTAATCTCAAAAGTATACCCGATGCGTAGCCATACC
GTTGCTGCAGAAGGGGGCTCCGCCGCTGTCGCGCAGGATCATGACAGCTTCGAATATCCCCNNNCCCCCGT
ACTAGTCGACGCCGTGAANANNNN

Figure 5-12

49G9-3 (12X)
fliP gene - putative structure; surface structures, flagellar biosynthesis

Transposon Tn10 Accession # AY528506
Nucleotide Accession # AE000287
Protein Accession # AAC75015

AACGTACCGGATCCGG
GATCATATGACAAGATGTGTATCCACCTTAACTTAATGATTTTTACCAAAATCATTAGGGGATTCATCAG
GGCGCAGCCGCTGCGTGAGTTTATGCTGCGTCAGACCCGTGAGGCAGATTTAGGGTTGTTTGCCAG
ACTGGCGAATATCGGCCCGTTGCGTNCTACTCNACNCGTGCCNATGCGCATTTTGCTNCCNGCCTA
CGTGACCAGCGAGTTGAAAACCGCATTTCAGATACGGCTTCACAGATTTTCATCCCTTTTTTGATTA
TCGACCTGGTGATAGCCAGCGTGTTGATGGC

Figure 5-13

51B12-3 (6X)
fliM gene - flagella gene, flagella biosynthesis; motor switch

Transposon Tn10 Accession # AY528506
Nucleotide Accession # AE000286
Protein Accession # AAC75012

ATGAAAACGNNCCGGATCCGG
GATCATATGACAAGATGTGTATCCACCTTAACTTAATGATTTTTACCAAAATCATTAGGGGATTCATCAG
TACTCAACTTCCAGCGGATTAATCGCCTTCCAGGCGTCGCTATAGCCTTCAAGCGCCAGTTTCAAC
ATGCGGTTGATGACGCGCTGTTCGGTATGGGTAAACTCGCGACCTTCCACTTTGGTCGGGAAGCGT
CCATCGCCGCCAAACAGGTTATCCACGGCGATAAACACCAGACTCGGTGAGAA

Figure 5-14

57E7-6 (7X)
fliP gene - flagella gene, putative surface structure, flagella biosynthesis

Transposon Tn10 Accession # AY528506
Nucleotide Accession # AE000287
Protein Accession # AAC75015

CGTACCGGATCCGG
GATCATATGACAAGATGTGTATCCACCTTAACTTAATGATTTTTACCAAAATCATTAGGGGATTCATCAG
GGCGCAGCCCGCTGCGTGAGTTTATGCTGCGTCAGACCCGTGAGGCAGATTTAGGGTTGTTTGCCA
GACTGGCGAATACCGGCCCGTTGCAGGGACCTGAAGCCGTGCCGATGCGCATTTTGCTCCCGGCCT
ACGTGACCAGCGAGTTGAAAACCGCATTTCAGATAGGCTTCACGATTTTCATCCCTTTTTTGATTAT
CGACCTGGTGATAGCCAGCGTGTTGATGGCATTGGGGATGATGATGGTT

Figure 5-15

61G2-3 (10X)
255 bp down stream of flhB gene

Transposon Tn10 Accession # AY528506
Nucleotide Accession # U88319
Protein Accession # AAC17834

NGNNNATACGNCCGGATCCGG
GATCATATGACAAGATGTGTATCCACCTTAACTTAATGATTTTTACCAAAATCATTAGGGGATTCATCAG
TATTAAGCGTGAATGATGCCAGAGCGCAAAGCGTTCAATGGTTTGAGTAAGGGGCAAAACAGGCG
GGATTTAGGGCTTTTGCTGCCACATATCCNNNNNNNNNGTACTAGTCGACGCGTGGCCA

Figure 5-16

63A9-1 (4X)
rfaQ gene (complement) – enzyme, macromolecule metabolism, LPS; LPS core biosynthesis

Transposon Tn10 Accession # AY528506
Nucleotide Accession # NC_002695
Protein Accession # NP_312534

AAACGGNCCGGATCCGG
GATCATATGACAAGATGTGTATCCACCTTAACTTAATGATTTTTACCAAAATCATTAGGGGATTCATCAG
TATGTGTACCGTGTATTGGCGCTAAGNGTGNGAAGCTTTTTTTCCAANTACCATGCTTGCCNNATG
ACCATAANGTTGCGATATNTTCATTCCGTGCATGCAAACANCGTACCNNCAGCGCCACCATNCAAC
TGATGCGTCNGANTAATGACCAGGTTNTANTTATTCTNTCGCCCGAGCCTCATCANCNAANGCTCN
CTTTNTNNNCGGNANNNNNATTTTNCCCNGTCTNNNTNTTGNTTNANTNNNTTACGCGGCNACNNA
TTNGTTNTGGTCNTACGNGCNNNATAACNGCNNCTCNCNNNCC

Figure 5-17

64F2-1 (9X)
factor Sigma32 – promoter dnaKp2; documented +1 site at 12121

Transposon Tn10 Accession # AY528506
Nucleotide Accession # D10765
Protein Accession # BAA01595

CGNCGGATCCGG
GATCATATGACAAGATGTGTATCCACCTTAACTTAATGATTTTTACCAAAATCATTAGGGGATTCATCAG
CGTTTCGCCCCTATTACAGACTCACAACCACATGATGACCGAATATATAGTGGAGACGTTTAGATG
GGTAAAATAATTGGTATCGACCTGGGTACTACCAACTCTTGTGTAGCGATTATGGATGGCACCACT
CCTCGCGTGCTGGAGAACGCCGAAGGCGATCGCACCACGCCTTCTATCATTGCCTATACCCAGGAT
GGTGAAACTCTAGTTGGTCAGCCGGCTAAACGTCAGGCAGTGACGAACCCGCAAAACACTCTGTT
TGCGATTAAACGCCTGATTGGTCGCCGCTTCCAGGACGAAGAAGTACAGCGTGATGTTTCCATCAT
GCCGTTCAAAATTATTGCTGCTGATATCCCNCCCCCCNG

Figure 5-18

66F4-3 (10X)
fliM gene - flagella biosynthesis, motor switch

Transposon Tn10 Accession # AY528506
Nucleotide Accession # AE000286
Protein Accession # AAC75012

TACCGGATCCGG
GATATATGACAAGATGTGTATCCACCTTAACTTAATGATTTTTACCAAAATCATTAGGGGATTCATCAG
CTTCAAGCGCCAGTTTCAACATGCGGTTGATGACGCGCTGTTCGGTATGGGTAAACTCGCGACCTT
CCACTTTGGTCGGGAAGCGTCCATCGCCGCCAAACAGGTTATCCACGGCGATAAACACCAGACTC
GGTGAGAACACCACCAGCCCAGTGCCGCGCAGCGGTTTCAGATGGATAAGGTTCAGGTTGGTCGG
CACCGGCAGGTTGCGGGCAAATT

Figure 5-19

67C8-4 (6X)
fliM gene - flagella biosynthesis, motor switch

Transposon Tn10 Accession # AY528506
Nucleotide Accession # AE000286
Protein Accession # AAC75012

NNCGTNCGG
GATATTGACAAGATGTGTATCCACCTTAACTTAATGATTTTTACCAAAATCATTAGGGGATTCATCAG
CGCTTGAAGGCTATAGCGACGCCTGGAAGGCGATTAATCCGCTGGAAGTTGAGTACGTGCGTTCG
GAAATGCAGGTGAAATTTACCAATATCACCACCTCGCCGAACGACATTGTGGTTAACACGCCGTTC
CATGTGGAGATTGGCAACCTGACCGGCGAATTTAATATCTGCCTGCCATTCAGCATGATCGAGCCG
CTACGGGAATTGTTGGTTAACCCGCC

Figure 5-20

67C9-6 (8X)
fliM gene - flagella biosynthesis, motor switch

Transposon Tn10 Accession # AY528506
Nucleotide Accession # AE000286
Protein Accession # AAC75012

ANCCGATCCGG
GATATATGACAAGATGTGTATCCACCTTAACTTAATGATTTTTACCAAAATCATTAGGGGATTCATCAG
CGCTTGAAGGCTATAGCGACGCCTGGAAGGCGATTAATCCGCTGGAAGTTGAGTACGTGCGTTCG
GAAATGCAGGTGAAATTTACCAATATCACCACCTCGCCGAACGACATTGTGGTTAACACGCCGTTC
CATGTGGAGATTGGCAACCTGACCGGCGAATTTAATATC

Figure 5-21

67E10-5 (6.5X)
fliI gene –Enzyme, flagella synthesis; surface structures, flagellum specific ATP synthase

Transposon Tn10 Accession # AY528506
Nucleotide Accession # AE000286
Protein Accession # AAC75008

CGNCCGGATCCGG
GATCATATGACAAGATGTGTATCCCCTTAACTTAATGATTTTTACCAAAATCATTAGGGGATTCATCAG
CACCCTGCATTCGCAGGAGCGGAGAAACATCCGCCGGAGCGGCAATCACCACTGAGCGTGCACGCCCTTCG
GCACCGAGGATGTTCTCAATAAAATCTTTTACTTCGCGCCCACGTTCACCAATCAAACCCACGACAATGATA
TCCNNNNNNNNNGTACTAGTCGACGCGTGGCCAAT

Figure 5-22

70G12-5 (5X)
flil gene – flagella synthesis, enzyme: surface structures; flagellum specific ATP synthase

Transposon Tn10 Accession # AY528506
Nucleotide Accession # AE000286
Protein Accession # AAC75008

TANGAAAAACGTACCGGATCCGG
GATCATATGACAAGATGTGTATCCACCTTAACTTAATGATTTTTACCAAAATCATTAGGGGATTCATCAG
CGCTCCAGCCCCTGGAGAGACGCTTNCCAGTCCGCGCGTTCAAAAATGCCTTGTTGCAAATAGCCCTCCAG
CTGCGGCCACAGGGCGATGGCTTTATCGAGCATCGGATCGCTGCCTTTGGCATACGCGCCGACGCTAACCA
GATCGCGGTTACGCTGAAAACTCGACAACAGCTGTTTGAAGGTGCGCACTCGCGCGTAATGTTGCTCACTG
ATCAACGCCGTCATTGCGCGGCTGATCGACGCTTCAATATCCNNNNNCNNNGTACTAGTCGACGCGTGGCC
A

Figure 5-23

71A4-3 (10X)
Downstream of rfaQ gene

Transposon Tn10 Accession # AY528506
Nucleotide Accession # M80599
Protein Accession # NP_418089

AGCNCGCCGGACNTCCCGGATCCGG
GATCATATGACAAGATGTGTATCCACCTTAACTTAATGATTTTTACCAAAATCATTAGGGGATTCATCAG
AGTCGCTAGTGGAAAAGCCATTTCGAAAAATCCTGGTCATAAAGATGCGATATCCCCCCACCGCGT
ACTAGTCGACGCGTGGCCANANANNNNNNNCGGCANNNCCNCCCNT

Figure 5-24

74B5-2 (2.5X)
rfaG gene (complement)- enzyme, macromolecule metabolism, LPS; glucosyltransferase I, LPS core biosynthesis

Transposon Tn10 Accession # AY528506
Nucleotide Accession # S75736
Protein Accession # AAD43826

ATACCCGATCCGG
GATCATATGACAAGATGTGTATCCACCTTAACTTAATGATTTTTACCAAAATCATTAGGGGATTCATCAG
CGCATTGCATCAACAGTTGCCGCACGGGGCCACCATGTTCGGGTATATACACAGTCGTGGGAAGG
CGATTGCCCGAAAGCATTTGAGCTTATTCANGNGCCAGTTAAGTCCCNTACCAACCATGGACGCAA
TGCAGAATATTATGCCTGGGTACAAAATCATNTNAAACAGCNTCCCNCAGGATCTGTGTCGNNGN
GTTCAATTATTATNCCCTCGNCNGGATTATCTTATTTGCCTGCTNAATGTCNGTCTTCTNATTCCTA
AATNT

Figure 5-25

76F11-2 (5.5X)
fliM gene - flagella gene, flagella motor switch biosynthesis

Transposon Tn10 Accession # AY528506
Nucleotide Accession # AE000286
Protein Accession # AAC75012

NGAAAACGGNCCGGATCCGG
GATCATATGACAAGATGTGTATCCACCTTAACTTAATGATTTTTACCAAAATCATTAGGGGATTCATCAG
CGCTTGAAGGCTATAGCGACGCCTGGAAGGCGATTAATCCGCTGGAAGTTGAGTACGTGCGTTCG
GAAATGCAGGTGAAATTTACCAATATCACCACCTCGCCGAACGACATTGTGGTTAACACGCCGTTC
CATGTGGAGATTGGCAACCTGACCGGCGAATTTAATATCTGCCTGCCATTCAGCA

Figure 5-26

77A5-2 (11X)
b1936 gene - orf; unknown function; hypothetical protein

Transposon Tn10 Accession # AY528506
Nucleotide Accession # NC 000913 (genome)
Protein Accession # E64957

CNCGATCCGG
GATCATTGACAAGATGTGTATCCACCTTAACTTAATGATTTTTACCAAAATCATTAGGGGATTCATCAG
ATTCAGGTGCGTAATAAGCTGGTGGCGGCGTATCAGGAAGTGATGAGCATGCAGGTGTAGGTTTT
GTAACCTGTTGTTAATTACATCCGATCTCACCGCGTGGGGCATGGATGGGGCAAACTCACTCAATT
TCTGGTTTAAAATGGATACCTGATCCTGAACGTTTTCTGCCATCCACGATCCGTATACGCGATAAC
CCCCCTGAACATCAGAGCGTCTCA

Figure 5-27

78E3-2 (7X)
fliA (complement) - flagella biosynthesis, alternative sigma factor

Transposon Tn10 Accession # AY528506
Nucleotide Accession # AE000285
Protein Accession # AAC74989

NAAAACGNCCGGATCCGG
GATCATATGACAAGATGTGTATCCACCTTAACTTAATGATTTTTACCAAAATCATTAGGGGATTCATCAG
GGGTTAATACCAGTTTTTCGCGCTCCGGCAACGTTTCGATGGCTTCCATCACCCGCTGGCGCAGAT
TACTGTCCAGTAGTTGTTGTAGCGGGTTTTCTCGCTGATGATCATCAGTAACCAGTTCGATGCTATC
GCCGTGCTCTTCGCGCCACTCATCGTAGGAGAAGAGCTGGCTGTTATTGGTGTCGAGCAACATTTG
GCGATAATCGGCAATATCNNCCCCCCCCGTACTAGTCGACGCGTGGCCAA

Figure 5-28

78F6-3 (2X)
tolA gene - membrane; colicin-related functions; membrane spanning protein required for outer membrane integrity

Transposon Tn10 Accession # AY528506
Nucleotide Accession # AE000177
Protein Accession # AAC73833

ATACNCGACCGG
GATCATATGACAAGATGTGTATCCACCTTAACTTAATGATTTTTACCAAAATCATTAGGGGATTCATCAG
AGTTTAGCTGCTGCCAACGCAGCCTGACAAAGTGCGGGATCGCCACCTTCAGGTTTGATATCCAGT
AACATACCATCGGGTGCCAGTTTTATGCGCAGCGTACAGGTTTTGCCTGCATAGGACGATGCGTCA
TAGAACTTACTTTCGATAGCAGATTTAATCTGCCCGGCATAGTTATTGATATCCNCCCCCCNNGTA
CTAGTCGACGCGTGGCCANNTATTCNGATATCNCNCCNGCCNGTCTANTCCCNCGTGGNCATATCT
GATNC

Figure 5-29

85G11-1 (6.5X)
Between 2 promoters (complement) - 1) factor sigma 70; predicted +1 site at 201135 and 2) factor sigma 70; predicted +1 site 2011238

Transposon Tn10 Accession # AY528506
Nucleotide Accession # D89826
Protein Accession # AAC75005

ANNGNAANAGCNCGCCGGACATCCCGGATCCGG
GATCATATGCACAAGATGTGTATCCACCTTAACTTAATGATTTTTACCAAAATCATTAGGGGATTCATCAG
AGTCTTGNTCCACTTTGCCAATANCGCCGGCCNTAGCNCTAGNCGNCGCACGNNCAGACGCGTGG
CCA

Figure 5-30

89A8-3 (6.5X)
fliG gene - flagella structural; flagellar motor component

Transposon Tn10 Accession # AY528506
Nucleotide Accession # AE000286
Protein Accession # AAC75006

CGNTACCGGACCGG
GATCATATGACAAGATGTGTATCCACCTTAACTTAATGATTTTTACCAAAATCATTAGGGGATTCATCAG
TGCTCGGCTCCTTTCAGCGCGATCAACAGCGATTCGGAATCCACTTCCTGCAACAGACGCTGAATG
CTGCGATCGTCGACATCCACCAGATTCTCGAACAGGAACATCTCGTCGATGATTTTCTGCGCCAGC
TCGCCGTCGAATTCACGCACGGCGGTAATAACGGCTTCTTCCTGCTGAGTTTTC

Figure 5-31

92G7-3 (3.5X)
rnhB gene – enzyme; degradation of RNA; product is RNAse HII, degrades RNA of DNA-RNA hybrids

Transposon Tn10 Accession # AY528506
Nucleotide Accession # AE000127
Protein Accession # AAC73294

GGAAAAAACGTCCGGATCCGG
GATCATATGACAAGATGTGTATCCCCTTAACTTAATGATTTTTACCAAAATCATTAGGGGATTCATCAG
GGTTGGGTACCCTTTGTGTTGGGCAAAACCATATTGCGGGAAAACAATATCCAGCGCCGCCNTTNN
NGCGTCACGCGTNACTTTCGCCAGGATAGACGCGGCACTGATTTCCGGTACGCGGCTATCGCCTTT
CACCACAGCCATCGCAGGCATCGGTAATTTCGGGCAGCGGTTACCATCAATCAACACATATTCCGG
CGCAATATGCAGCCCAGCGACGGCACGCTGCATCGCCAGCATGGTCGCATGAAGAATGTTCAGCT
CGTCGATATCCNNNNNNCNCGTACTAGTCGACGCGTG

Figure 5-32

92G9-1 (3.5X)
rnhB gene – same clone as above

Transposon Tn10 Accession # AY528506
Nucleotide Accession # AE000127
Protein Accession # AAC73294

TANGAAAAAAACGTTCCGGATCCGG
GATCATATGACAAGATGTGTATCCACCTTAACTTAATGATTTTTACCAAAATCATTAGGGGATTCATCAG
GGTTGGGTACCCTTTGTGTTGGGCAAAACCATATTGCGGGAAAACAATATCCNCCNCCCNNGTACT
AGTCGACGCGTGGCCAAATATNNNNATATNNNNNNNNNNNNNNCTANNNNNCNCGNGGNNANNN
N

Figure 5-33

94G6-3 (4X)
Downstream of rfaQ gene

Transposon Tn10 Accession # AY528506
Nucleotide Accession # M80599
Protein Accession # NP_418089

NNNGNAAAGCCCGCCGGACNTCCCGGATCCGG
GATCATATGACAAGATGTGTATCCACCTTAACTTAATGATTTTTACCAAAATCATTAGGGGATTCATCAG
AGTCGCTAGTGGAAAAGCCATTTCGAAAAATCCTGGTCATAAAGATGCGATATCCNGNNNCCNNG
TACTAGTCGACGCGTGGCCAAAANNNCNNNNNNNANNNCNATNCTNGCNCCCNNCCANC

Figure 5-34

98E7-4 (6X)
fliR gene - putative enzyme, surface structures; flagellar biosynthesis

Transposon Tn10 Accession # AY528506
Nucleotide Accession # AE000287
Protein Accession # AAC75017

CGACCGGATCCGG
GATCATATGACAAGATGTGTATCCACCTTAACTTAATGATTTTTACCAAAATCATTAGGGGATTCATCAG
CACTGAATCTGGCATTAGGTTTACTTAATCGTATGGCCCCGCAATTATCCATTTTTGTTATTGGATTTCCATT
AACTCTGACTGTCGGCATCTCTTTAATGGCGGCATTAATGCCGTTAATTGCACCTTTTTGCGAACATTTATTC
AGTGAAATTTTTAATTTGCTGGCTGATATTATTAGTGAATTGCCATTAATATAATTCCGTAACGTTTATCATG
TTATCCTAAGGATTATCCGAAAAATAATACCTACGAACATCTTCCAGGATACTCCTGCAGCGAAATATTTGT
TTTAAGCTCACTCACATATCCCNCCCNCCNGTACTAGTCGACGCGTGGCCA

Figure 5-35

98E11-3 (5X)
flgH gene - structural component, surface structure; flagellar biosynthesis, basal body outer-membrane L (LPS layer) ring protein

Transposon Tn10 Accession # AY528506
Nucleotide Accession # AE000208
Protein Accession # AAC74163

AACNAAACGGNTNCGGCATCGG
GATCATATGACAAGATGTGTATCCACCTTAACTTAATGATTTTTACCAAAATCATTAGGGGATTCATCAGC
GCTGCGCATACTTATGCCATATCCNNCNNGNNGGTACTAGTCGACGCGTGGCCANATTNNNNNAT
CNNCNNNNNNGGGGCNNN

Figure 5-36

98G12-4 (5X)
mdoG gene – enzyme, osmotic adaptation; periplasmic glucans biosynthesis protein

Transposon Tn10 Accession # AY528506
Nucleotide Accession # AE000206
Protein Accession # AAC74132

AAACGACCGGACCGG
GATCATATGACAAGATGTGTATCCACCTTAACTTAATGATTTTTACCAAAATCATTAGGGGATTCATCAG
GGGGCAAGTTGCTTTTGGGCGTCTCGTAGCCTTTCCCGGCTAAAGATTGAGCTTGCTTTGCGACAT
CATCAATACTGAAAGCCCAGCTTGAAGATGTATACAGGGTTAACATTACTGCAGCACTCAACCAA
CGCATTTTCATTATTTGTAGCTTATGTTTCATAATTAGTAAGGCACTTCCCCCTTTNGTGTGCTTATA
TCCCTNNGNTNNCNTNCTAGTCNACNCGTGGCCACTNCTATCCNGNNNTCCCCGNTNNGCAGTANT
CAGAC

Figure 5-37

103C8-4 (9X)
fliP - flagella biosynthesis, surface structure

Transposon Tn10 Accession # AY528506
Nucleotide Accession # AE000287
Protein Accession # AAC75015

GANNAAACGACCGGATCCGG
GATCATATGACAAGATGTGTATCCACCTTAACTTAATGATTTTTACCAAAATCATTAGGGGATTCATCAG
GGCTGCGCCCCTTTTTCCAGCGCCTCCTGCATTGATATTTTCTCTTCGCTGAATGGCTGGTACGCAT
CTACATAAATTTTGTCGATCACCGGTGACATAATAAAAAAGGTCAAAAACAGTGCCAGCCCCAGC
AATACCTGGTTAGGTGGCGCGGAGGGTGTTCCCAGCGCGTTACGCAATAAACCAAAAACAATGAT
GATGCGGGTGAAACTGGTCATCATCAGTAAAATTGCCGGAATAAACGTCAACGAGGTGATGAACA
CCAGCGTCTGCACCGGGAGCGACCAGCTTTGTCCACCGCCAGGCAGCG

Figure 5-38

103E8-4 (7X)
yojN - putative regulator, not classified; product is putative 2 component sensor protein

Transposon Tn10 Accession # AY528506
Nucleotide Accession # AE000310
Protein Accession # AAC75276

NATACGNCCGGATCCGG
GATCATATGACAAGATGTGTATCCCCTTAACTTAATGATTTTTACCAAAATCATTAGGGGATTCATCAG
GGTGCAACCTGTATCACACCCGATGAAAGATTAATTAGTCAAGATTATGATATCTTTTTAACGGAT
AATCCGTCTAATCTTACTGCCTCTGGCTTGCTTTTAAGCGATGATGAGTCTGGCGTACGGGAAATT
GGGCCTGGTCAATTGTGCGTCAACTTCAATATGAGCAACGCTATGCAGGAAGCGGTCTTACAATTA
ATTGAAGTGCAACTGGCGCAGGAAGAGGTGACAGAATCGCCTCTGGGCGGAGATGAAAATGCGC
AACTCCATGCCAGCGGCTATTATGCGCTCTTTGTAGACACAGTACCGGATGATGTTAAGAGGCTGT
ATACTGAAGCAGCAACCAGTGACTTTGCTGCGTTA

Figure 5-39

104G4-5 (2.5X)
Between mreB and yhdA genes (complement). mreB: phenotype, cell division; regulator of ftsI, penicillin binding protein 3, septation function. yhda: orf, function unknown, hypothetical protein, 1232 bp upstream of mreB

Transposon Tn10 Accession # AY528506
Nucleotide accession # M22055
Protein Accession # AAA83892

ANNNNCGATCCGG
GATCATATGACAAGATGTGTATCCACCTTAACTTAATGATTTTTACCANAATCATTAGGGGATTNATCAG
CTNAATGCATGCNCNACCATTGCCTCNGCTGTTTGCAACCGNGTAAGGNGCATTCATNTGCATATG
TTGCTGCNANCAATCTGGCTGAGNAGACAAGCNCACTCCCATGANACGCATCGCGCATTATTNTAC
GTGAAANCGGATNNAANGGNTGGNTAAACCNANGANCCNNCGCCGANTATNNTTCCNCTGNCAN
NCTNANNTNGNCTNGNACNGANNNCNANNCNACNCCTCTTTNTNNNNTTCCGNTNNNGNNGNNNN
NNNTNGTNNTCCNNCCTGTNTNCANNTNNCNNNGNTCNTNCNCCCNTCTNTCCANTGCCANTTGTN
NCNAGGTNCGATNTCTGCNGACCNACNNNNTAGNANCCNN

Figure 5-40

107B12-2 (2.5X)
Upstream of promoter - factor sigma 70; predicted +1 site at 3806141

Transposon Tn10 Accession # AY528506
Nucleotide Accession # M80599
Protein Accession # AAC17834

GNAAANCCCGCCGGACATCCCGGATCCGG
GATCATATGACAAGATGTGTATCCACCTTAACTTAATGGATTTTTACCAAAATCATTAGGGGATTCATCAG
GCGGTAGCGTGCTTTTTTCTGCTTAACTTAACCAGACAATCACACAAAAGAGTCGCTAGTGGAAAA
GCCATTTCGAAAAATCCTGGTCATAAAGATGCGATATCCNNNNNNN

Figure 5-41

110E8-3 (6X)
fliP gene – Putative surface structure, flagellar biosynthesis

Transposon Tn10 Accession # AY528506
Nucleotide Accession #AE000287
Protein Accession # AAC75015

AACGCTNCCGATCCG
GATNATATNAACAGATNTGTATNCACCTTATCTTAATGANATTTTACCANAATCATATTGGGGATATCATAT
ANGGGCTGCCCCCTTTTTCCAGCCCCTACTGCATTGATATTTTNTCTTCGNTGNAT
GGCTGGTACGCATCTACATAANTNTTGACGATCACCGGTGACNTAATAAAANAG
GNCNNANNCANTGCCANTCCCAGCAATNCNTGGTTNNGTGGNGCGGACGGTGCT
NCCATNGCNNGACNCACNNAACCNANNNCNATGANGNTNCCNCNGANANTGGA
NATCATCCTGCAANNCNACNGNATNCNNA

Figure 5-42

110F12-2 (9X)
Between flhD and insB_5 genes (complement)

Transposon Tn10 Accession # AY528506
Nucleotide Accession # U88319
Protein Accession # AAC17834, AAC74963

CGNCCGGATCCGG
GATCATATGACAAGATGTGTATCCACCTTAACTTAATGATTTTTACCAAAATCATTAGGGGATTCATCAG
CGATNANCTGCAATAAGCAGAACCNCCTTTTTGGNTTAATATGTCCTTACAAATAGAAATGGGTCTTTACAC
TTATCTAAGATTTTTCCTATATCNNCNCNCCNNGTACTAGTCGACGCGTGGCCATTTATNNNNNATNTCCTN
NTNGTCTCNNGNNCNNCNCGCGGCCNCANCNNNATATNNNTNNNNCNCTNCACTCTN

Figure 5-43

111G8-1 (4X)
flgK gene – structural component, flagella biosynthesis; hook-filament junction protein 1

Transposon Tn10 Accession # AY528506
Nucleotide Accession # AE000209
Protein Accession # AAC74166

AACCCGATCCGG
GATCATATGACAAGATGTGTATCCACCTTAACTTAATGATTTTTACCAAAATCATTAGGGGATTCATCAG
GGCTGGGTTGGCAATGGTGTCTACGTTTCTGGTGTGCAGCGTGAGTATGATGCGTTTATTACCAAC
CAGTTACGTGCGGCGCAGACGCAAAGTAGCGGTCTGACTGCCCGCTATGAGCAGATGTCGAAAAT
CGACAATATGCTCTCCACCAGTACCTCTTCGCTGGCAACACAGATGCAGGATTTCTTCACCAGCCT
GCAAACGCTGGTGAGTAACGCGGAAGACCCGGCAGCGCGCCAGGCGCTGATTGGGAAATCAGAA
GGATTGGTGAATCAGTTTAAAACCACCGATCAATATCNNCNNNNCCCGTACTAGTCGACGCGTGG
CCANANNATNCT

Figure 5-44

115A3-5 (2.5X)
fliD gene – flagella biosynthesis, surface structure; filament capping protein, enables filament assembly

Transposon Tn10 Accession # AY528506
Nucleotide Accession # AE000285
Protein Accession # AAC74991

ATACCNGATCCGG
NTCATATGACAAGATGTGTATCCCCTTAACTTAATGATTTTTACCAAAATCATTAGGGGATTCATCAG
GCTTACGCCTGCTTTTGCGTTGTTGATGGCATCACGGATCCCGCTTAACGATGAGTTAGCCGCGCT
GATATCAATGGTNATCGTACTANTCGACGCGTGGCCATGAATGGTGAGTTTACTGTCGCTGGTGGC
GATCGCCGTTTTCATATCGNCNNTTNCNGTACTAGTCGACGCGTGGCCAAATTNNTNTNANAAAAA
TTCN

Figure 5-45

115B7-6 (7X)
flgB gene – flagella biosynthesis, cell-proximal portion of basal-body rod

Transposon Tn10 Accession # AY528506
Nucleotide Accession # AE000208
Protein Accession # AAC74157

AACGGTTACCGGATCCGG
GATCATATGACAAGATGTGTATCCACCTTAACTTAATGATTTTTACCAAAATCATTAGGGGATTCATCAG
CGCGCGATATCGATTTTGCCAGTGAACTTAAAAAAGTCATGCAACGTGGACGGGATGCAACCAGT
GTGGTTGCACTGACGATGACCTCAACGCAACACATTCCGGCGCAGGCGCTGACGCCTCCTACCGCA
GAACTGCAATACCGTATTCCGGACCAGCCTTCGCTTGACGGTAATACCGTCGATATGGATCGCGAA
CGCACCCAGTTTGCCGATAACAGCCTGCAATACCAGATGAGCCTTAGCG

Figure 5-46

122F6-1 (4X)
fliL gene - flagella gene; putative surface structure

Transposon Tn10 Accession # AY528506
Nucleotide Accession # AE000286
Protein Accession # AAC75011

CGNTACCGGATCCGG
GATCATATGACAAGATGTGTATCCACCTTAACTTAATGATTTTTACCAAAATCATTAGGGGATTCATCAG
CACGACGCGTTGCTGCGCTTTGTCGTCAGCGGCAACCTGATGCGAATGCCAGTAGCTGTAACCTGC
GCTGGCACAGGCCGCGAGGGTAATGAATACCAGAATCGGGATCCAAAGCGATCGCTTGCTTTTCTT
GCTTATCGCGTAATCAGTCATGTGTTGCGGTCTTCCTGTGTCGCTACTGCTTATC

Figure 5-47

123B8-4 (3.5X)
rfaQ gene (complement) – Macromolecule metabolism, LPS; LPS core biosynthesis

Transposon Tn10 Accession # AY528506
Nucleotide Accession # NC_002695
Protein Accession # NP_312534

AAACGACCGGATCCGG
GATCATATGACAAGATGTGTATCCACCTTAACTTAATGATTTTTACCAAAATCATTAGGGGATTCATCAG
CGCTAAGTGTGTGAAGCTTTTTTTCCAAATACCATGCTGCCGATGACCATAAAGTTGCGATATTTTC
ATCCGTGCAGGTAAACAACGTACCAGCAGCGCCACCATCCACTGATCCGTAAGATTAATGACCAG
GTCATAATTATTCGCACGCAGAGNTTTTATCAACNAAAGCACATTTTTAATTTNATCGAAAGTTCC
CNCNCCTTTATTGCTTANCCCATAGAGCGCANTNNTTTCCGGGTTTNCANACAAAATNTGGATGGT
GNCCTGNCNAAGCNNCANGTCTANNTNNGCTNTATGAGAATCTG

Figure 5-48

123E4-3 (6.5X)
fliR gene – putative enzyme; flagella biosynthesis

Transposon Tn10 Accession # AY528506
Nucleotide Accession # AE000287
Protein Accession # AAC75017

AAACGACCGGATCCGG
GATCATATGACAAGATGTGTATCCACCTTAACTTAATGATTTTTACCAAAATCATTAGGGGATTCATCAG
AGTTTTACCCGTTTCGGTACGCTGCGTTCGCTCAGAATCGGCGCGGTGGAGATCATCGCCAGCTCN
CGCANTNACGGNCAGAANTACAGGTTTAACCAGGATAGCCATTGTTNGCTTGCCACCTGCANCAT
AGTACGGTTACCCNATGATTTACTNGNAGGTTAGTGAACAANGTGCGGNCAGTNATTCANCAACA
CATTNNGCATGNTCTGTCTNGGCANNTATTTTGGTGATNAANANGGCCGATNNTTTTNCGANTNNC
CGNNNTGGGNTNCTTNTTCATCNAGTNNCNNATGGGCGNGTATN

Figure 5-49

125C9-2 (7X)
fliP gene – Putative surface structure, flagella biosynthesis

Transposon Tn10 Accession # AY528506
Nucleotide Accession # AE000287
Protein Accession # AAC75015

TACGNCCGATCCGG
GATCATATGACAAGATGTGTATCCACCTTAACTTAATGATTTTTACCAAAATCATTAGGGGATTCATCAG
GGCTGCGCCCCTTTTTCCAGCGCCTCCTGCATTGATATTTTCTCTTCGCTGAATGGCTGGTACGCATCTACAT
AAATTTTGTCGATCACCGGTGACATAATAAAAAAGGTCAAAAACAGTGCCAGCCCCAGCAATACCTGGTTA
GGTGGCGCGGAGGGTGTTCCCAGCGCGTTACGCAATAAACCAAAAACAATGATGATGCGGGTGAAACTGG
TCATCATCAGTAAAATTGCCGGAATAAACGTCAACGAGGTGATGAACACCAGCGTCTGCACCGGGAGCGA
CCAGCTTTGTCCACCGCCAGGCAGCGGCTGGCTGGTGATACCCGGCAGTTGCGCGAAGGCGAGGGGCGTAA
TCAGCCAGAGAAGGACAGGTGCGACAGACAATAAACGACGCAT

Figure 5-50

125F2-4(3.5X)
rfaQ gene (complement) – enzyme; macromolecule metabolism: LPS core biosynthesis

Transposon Tn10 Accession # AY528506
Nucleotide Accession # NC_002695
Protein Accession # NP_312534

GNGNAAAAACGTNCCGG
ATCCGGGATCATATGACAAGATGTGTATCCACCTTAACTTAATGATTTTTACCAAAATCATTAGGGGATTCATCAG
GATGGTGTCCTGATAAAGCAGCATATCGATTTTTGCATCANGATAATTCTGCTTGAGCGTACTGAT
GACAGGAGTAGTTAATAACATATCCCCATGATATCNNCNNNNCNNGTACTAGTCGACGCGTGGCC
A

Figure 5-51

126G2-2 (7X)
flhA (complement) - flagella biosynthesis; possible export of flagella proteins

Transposon Tn10 Accession # AY528506
Nucleotide Accession # AE000281
Protein Accession # AAC74949

CGNCCGGATCCGG
GATCATATGACAAGATGTGTATCCCCTTAACTTAATGATTTTTACCAAAATCATTAGGGGATTCATCAG
CCTGGTGCCTGGAATGCCGAACCTGGTATTTTTGCTGTTCACTGCCGGATTGCTCGGGCTGGCCTG
GTGGATACGCGGACGCGAACAAAAAGCGCCTGCCGAACCCAAACCGGTAAAAATGGCAGAGAAT
AATACCGTTGTCGAAGCGACGTGGAACGATGTACAACTGGAAGATTCTCTGGGAATGGAAGTGGG
TTAT
GGACTGATCCCGATGGTCGATTTCCAGCAGGATGGTGAGTTGTTGGGCCGTATACGCAGTATCCGC
AAG

Figure 5-52

126A3-2 (7X)
flhA gene (complement) - flagella biosynthesis, possible export of flagella proteins

Transposon Tn10 Accession # AY528506
Nucleotide Accession # AE000281
Protein Accession # AAC74949

ACGTNCCGGATCCGG
GATCATATGACAAGATGTGTATCCACCTTAACTTAATGATTTTTACCAAAATCATTAGGGGATTCATCAG
CCTGGTGCCTGGAATGCCCGAACCTGGTATTTTTGCTGTTCACTGCCGGATTGCTCGGGCTGGCCTG
GTGGATACGCGGACGCGAACAAAAAGCGCCTGCCGAACCCAAACCGGTAAAAATGGCAGAGAAT
AATACCGTTGTCGAAGCGACGTGGAACGATGTACAACTGGAAGATTCTCTGGGAATGGAAGTGGG
TTATCGACTGATCCCGATGGTCGATTTCCAGCAGGATGGTGAGTTGTTGGGCCGTATACGCAGTAT
CCGCAAGAAATTTGCCCAGGAGATGGGATATCN

Figure 5-53

132B8-2 (7X)
fliM gene - surface structures/flagellar biosysnthesis, component of motor switch/energizing

Transposon Tn10 Accession # AY528506
Nucleotide Accession # AE000286
Protein Accession # AAC75012

NTNNNAAAACACGCCGGACATCCGGATCCGG
GATCATATGACAAGATGTGTATCCACCTTAACTTAATGATTTTTACCAAAATCATTAGGGGATTCATCAG
CGCTTTGCCCGCCATTTTCGTATGGGGCTGTTCAACCTGCTGCGTCGTAGCCCGGATATATCCNCCN
GGNGCGTACTAGTCGACGCGTGGCCAANNNNNNNNCNNCNNCTAGCNNTAAAANNGNCATNANC
CNCNCNCACAANCACNNANGNANNCNTTNCNAAACNANCGTANNATANCCCCNNC

Figure 5-54

136E3-1 (7.5X)
arcB gene (complement) - enzyme, Global regulatory functions, aerobic respiration sensor- response protein; protein kinase/phosphatase, sensor for arcA

Transposon Tn10 Accession # AY528506
Nucleotide Accession # AE000400
Protein Accession # AAC76242

NNAAAGCCCGCCGGACATCCCGGATCGG
GATCATATGACAAGATGTGTATCCACCTTAACTTAATGATTTTTACCAAAATCATTAGGGGATTCATCAG
CGCAAAGCCTGCTTTGANATCCGTAAAGNGCGGACTAANCNACNCGNGGNCNAA

Figure 5-55

139G5-3 (5X)
rfaP gene – enzyme; macromolecule metabolism: LPS; phosphorylation of core heptose, attaches phosphate containing substrate to LPS core

Transposon Tn10 Accession # AY528506
Nucleotide Accession # AE000440
Protein Accession # AAC76654

GNGAAAAAAACGNACCGGATCCGG
GATCATATGACAAGATGTGTATCCCCTTAACTTAATGATTTTTACCAAAATCATTAGGGGATTCATCAG
GGTTAAATCCATTAACTCGCGCATCATTTATTATTACCGAAGATCTCACTCCCACAATTAGCCTTGAAGATT
ATTGTGCCGATTGGGCAGTCAACCCGCCTGATATCCNGNNCNNNNGTACTAGTCGACGCGTGGCCATANAN
TNAGCTCNTNCTACNNCCNNANTCCTATCCACCCGTGGCTNCAGNNANCATTCNGNNNACACCANTTACNN
NCCAGNCCNCNTCCCCCNGNNCTCNNCTACTCANNACTTCANNANANNATGNCNTTCNNNNGCNNNTCGNT
CNCCCACNACNNCNTTTNTTNCNNCCTCTNNCNANCTCNNCCNTNNCNCTNTNATTCCNCTTTTACCCTNAN

Figure 5-56

152B4-6 (9X)
flgI - flagella biosynthesis, putative surface structure; product is homologue to P-ring of flagella basal body in Salmonella

Transposon Tn10 Accession # AY528506
Nucleotide Accession # AE000208
Protein Accession # AAC74164

GNNGAACGNCGGATCCGG
GATATATGACAAGATGTGTATCCACCTTAACTTAATGATTTTTACCAAAATCATTAGGGGATTCATCAG
CACTTTGCATTGATTGCAGTATGGACATCAGATCCATCGGCGTAGCGCCCAGCGCATTGAGCGCGC
GCACCACGTTATTGAGGCTGGCGCTGGAACGTACGCTTTGCAGCGAACCGCCGCTCTGGCGTAAAT
CGATCTGCGTTTGTGGAGTAACCACAGTCTGTCCACCACCAAACGGTGTATCTGGCTGGCTGACAT
TGGCCTGACGATTAACTGTTACTGAGAGATTCCCCTGCGCTACCGCGCAGCTGTCGAGGGTCACTT
CGCGATTCATCACCACCGAACCGGTGCGCGAGTTAATCACTACTTTAGC

Figure 5-57

163E7-5 (4X)
fliD gene – flagella surface structure; capping protein (same clone as 1B10)

Transposon Tn10 Accession # AY528506
Nucleotide Accession # AE000285
Protein Accession # AAC74991

TNGNAAAAACGTNCCGGATCCGG
GATCATATGACAAGATGTGTATCCACCTTAACTTAATGATTTTTACCAAAATCATTAGGGGATTCATCAG
GGTCAGGTCTGGATTTAAGTTCCATCCTTGATAGCCTCACCGCCGCGCAAAAAGCGACGCTNACCC
CCATTTCAAATCAGCAATCGTCGTTTACCGCTAAACTTAGCGCCTACGGTACGCTGAAAAGCGCGC
TGACGACTTTCCAGACCGCCAATACTGCATTGTCTAAAGCCGATCTTTTTTCCGCCACCAGCACCA
CCAGCAGCACCACCGCGTTCAGTGCCACCACTGCGGGTAACGCCATCGCCGGGAAATACACCATC
AGCGTCACCCATCTGGCGCAGGCGCAAACCCTGACCACGCGCACCACCAGAGACGATACGAAAAC
GGCGATCGCCACCAGCGACAGTAAACTCA

Figure 5-58

163F3-5 (8X)
fliD gene – flagella surface structure; Capping protein

Transposon Tn10 Accession # AY528506
Nucleotide Accession # AE000285
Protein Accession # AAC74991

NNANNAACAATACGTCC
CAAGNANANNTGACNAGANGTGTATCCACCTTAACTTAATGATTTTTACCAAAATCATTAGGGGATTCATCNG
GGNCCGGTCTGGATTTAAGTTTCCATCCTTGATAGCCTCACCGCCGCGCAAAAAGCGACGCTAACC
NCCATTTCANATCAGCAATCGTCGTTTACCGCTAAACTTAGCGCCTACGGTACGCTGAAAAGCGCG
CTGACGACTTTCCAGACCNCCAATACTGCATTGTCTAAAGCCGATCTTTTTTCCGCCACCANCACC
ACCTGCAGCACCACNGCGTTCANTGCCNCCNCTGCGGGNNACNCCATCGCCNGGAAATACCCCAT
TACCGNTCANCCATCTGGCANATGCNGCNAACCCTTGAACACGC

Figure 5-59

167C2-3 (8.5X)
flgB gene – Structural component, flagella biosynthesis ; cell – proximal portion of basal body rod

Transposon Tn10 Accession # AY528506
Nucleotide Accession # AE000208
Protein Accession # AAC74157
AAAACGTCCGGATCCGG
GATCATATGACAAGATGTGTATCCACCTTAACTTAATGATTTTTACCAAAATCATTAGGGGATTCATCAG
CGCTCAATCTGCGCGCCCAGCGTCAGGAAGTGCTGGCAGCAAACATCGCCAATGCCGATACCCCT
GGTTATCAGGCGCGCGATATCGATTTTGCCAGTGAACTTAAAAAAGTCATGCAACGTGGACGGGA
TGCAACCAGTGTGGTTGCACTGACGATGACCTCAACGCAACACATTCCGGCGCAGGCGCTGACGC
CTCCTACCGCAGAACTGCAATACCGTATTCCGGACCAGCCTTCGCTTGA

Figure 5-60

1G3-6 (16X)
ycdQ gene (complement) - putative enzyme homologous to IcaA in Staphylococcus

Transposon Tn10 Accession # AY528506
Nucleotide Accession # NC_000913
Protein Accession # NP_415541

ATAAAACGGNTACCGGATCCGG
GATCATATGACAGATGTGTATCCACCTTAACTTAATGATTTTTACCAAAATCATTAGGGGATTCATGAG
GGCGCTGTTTCCACAGCCCTTTTAACGTTTCAGGCATTAATATCCAGCACAGTGNCCCTNGNNNNCNCNNN
NNCNTCCACTGATTCAACTGCAGCTTCCAGCTAATATCAATATCTTCGGTGATCATATNAGTCCACNCGGNN
CTAGTCGACGCGTGGCCANNANTNNNNCNTTNTTTNTNNCTN

Figure 5-61

11E4-3 (12X)
Immediately Upstream of promoter (factor sigma 70, predicted 1+ start site 1986220) and gene b1904 (orf, function unknown)

Transposon Tn10 Accession # AY528506
Nucleotide Accession # NA (Not Available)
Protein Accession # NA

TTTAAAAACCGGTTACCGGATCCGG
GATCATATGACAAGATGTGTATCCACCTTAACTTAATGATTTTTACCAAAATCATTAGGGGATTCATCAG
TGCCAGGCGTCTTTTCCGGCCATTGTCGCAGCACTGTAACGCGTAAAATAGTGCTTTCTCTTACTCTTCTGGC
TGGACCATGAGACTTCTGATTCTGACTCTTTCATTAATATCCNNNNCNNNNGTACTAGTCGACGCGTGGCCA
NANNANTNNTATNTTTNANNACNN

Figure 5-62

12F12-6 (23X)
ycdS gene (complement) – putative outer membrane protein

Transposon Tn10 Accession # AY528506
Nucleotide Accession # AE000204
Protein Accession # AAC74109

TTGAAAACCGCTCCGGATCCNG
GATCATATGACAAGATGTGTATCCACCTTAACTTAATGATTTTTACCAAAATCATTAGGGGATTCATCAG
CGTTAAATTGGCATCGTCATCGCGGCAGCAAGTTGATTATTACGTAATGCCTGCACGTAATTCTGTGGGATA
TCCNNCCCNNNCGTACTAGTCGACGCGTGGCCATNTNACNTNCNGCAATNCNTTCTGACACTTCNNNTTNC
TNTNNAT

Figure 5-63

14B7-4 (4X)
leuO gene –putative regulator; probable transcriptional activator for leuABCD operon; amino acid biosynthesis: Leucine

Transposon Tn10 Accession # AY528506
Nucleotide Accession # AE000118
Protein Accession # AAC73187

GCNNGCGGTAAACGNCCGGATCCGG
GATCATTGACAAGATGTGTATCCACCTTAACTTAATGATTTTTACCAAAATCATTAGGGGGATTCATCAG
AGTTAAGTGTGACAGTGGGAGTTAAGTATGCCAGAGGTACAAACAGATCATCCAGAGACGGCGGA
GTTAAGCAAACCACANCTTNCGNATGGNCGATTTCAACTTATTAACNCGTTTCGATGCCNTGNTGN
AGGAGCCNANCATTNTTCNCAGCCCGCTCATCGCCCTGGGAACCTTCNCCCCCCCTNCNTTCCTNT
GCTNGCCTTGGGGCCCCCNNCACNCAACGNAGACNGGGCCNATCCC

Figure 5-64

16C8-2 (24X)
Promoter (factor sigma 70, predicted 1+ start site 1986220); upstream of b1904 (orf, unknown function)

Transposon Tn10 Accession # AY528506
Nucleotide Accession # NA
Protein Accession # NA

AACCGTACCGGATCCGG
GATCATTGACAAGATGTGTATCCACCTTAACTTAATGATTTTTACCAAAATCATTAGGGGGATTCATCAG
TGCNACGNCNCTNTNANNNCCATNGATNTNGCACTGTAACGCGCTAAATAACGCTTGTNTCTTACT
CTTCTGGCTGGACCATGAGACTTCTGATTCTGACTCTTTCATTAATATCCCCCCNCNCCGTACTAGT
CGACGCGTGNCNATATTATGNNNCCNNNNNCTANTNNNC

Figure 5-65

24E12-4 (8.5X)
fucA gene (complement) - enzyme, degradation of molecules: carbon compounds: product is L-fuculose-1-phosphate aldolase

Transposon Tn10 Accession # AY528506
Nucleotide Accession # AE000363
Protein Accession # AAC75842

CNNCCGGATCCGG
GATCATATGACAAGATGTGTATCCACCTTAACTTAATGATTTTTACCAAAATCATTAGGGGATTCATCAGAG
GCAAGTGTCAATAATCTGACGAGCAAGTTTATTTCGTTCCATTAGCTACCTCTCTCTGATTCAAAAC
AGGGCAATAATGTTGTTCCTTTCACACTATTGAATTAGCCGTTTAATTACCCACCATCTTCTTCCTG
ATTAACAAGAAAGAAATTCACAAGCTTATAT

Figure 5-66

26G11-3 (8X)
ycdS gene - (complement), putative outer membrane protein

Transposon Tn10 Accession # AY528506
Nucleotide Accession # AE000363
Protein Accession # AAC74109

AACGNCCGATTCCG
GATCATATGACAAGATGTGTATCCACCTTAACTTAATGATTTTTACCAAAATCATTAGGGGATTCATCAG
CCAGATGCGTTCCTGACCCTCAAGTGAGACTTCATGACGCTGGTTACTGTCGGAAAAATCAGTGAA
AGCCCAGGAGACACCGTACTTACGCCGCTCATTTTGATACCAGCGAACATAAGCCTGAGCACTGTT
GCCTGTAACACCATTTTTCATTGCCCGTAATGGAACGCGGTGAGAGAGGCGTTCCAGTTGCGAACC
AATACGCCAGTTATCATTAAAATCATACCAGCCAGACAGGCGCGCGCCGGGTTTATGCTCATGATT
GAAAACGCGTTCAGCGTACTCTGCCTCGAGCCAGATATTACG

Figure 5-67

27F9-2 (2X)
Between promoter (factor sigma 70 predicted 1+ start site 4272977) and yjcC gene (orf; unknown function)

Transposon Tn10 Accession # AY528506
Nucleotide Accession # NA
Protein Accession # NA

AACGNNCCGGATCCGG
GATCATATGACAAGATGTGTATCCACCTTAACTTAATGATTTTTACCAAAATCATTAGGGGATTCATCAG
TGCCCAGGGTTTTCACCTTGCAATGGCCGGGTATAAACAGGCAGGAAATTGANANCANTGAGNCA
TNNNCNACGANACCAATTNCTGGCNTNGCCGGGCATTATCTTTTTAATTCTCTTTCCCATCATTCTT
TCGCTATGGATTGCCTTCCTTTGGGCAAAATCAGAAGTGAATAATCAGCTCCGAACCTTTGCTCAA
CTGGCACTGGATAAATCCGAGCTGGTCATT

Figure 5-68

31A4-4 (7X)
ycdS gene (complement) - putative outer membrane protein

Transposon Tn10 Accession # AY528506
Nucleotide Accession # AE000204
Protein Accession # AAC74109

CNCGCCGGACATCCGGATCCGG
GATCATATGACAAGATGTGTATCCACCTTAACTTAATGATTTTTACCAAAATCATTAGGGGATTCATCAG
GTGACAGTTAGCGCGCCCGGATAATTTTCACTCTCCAGGTGGCTGTAAAAGAGATCCGCAAGTTCT
TCATCGGATAAATCCGGGGCAATGGTCTCCTTGTGATAAAAGAGCTCGGTCATTATTGACTGTGCT
TTTTTCGGCTGATGATCTTTGAGATAAGCCGATGCAACCCAATATTGCCCCCAGGGCGGAATAATT
TGCCCCGTCTTTTTTAATCGCTGATAGTGAGAAATAACGTCTTTATAACGATCGCGAGTTAATAAC
GCGCCAAGATGATCAACCTGAATACGCTGGTACTGGGCAGTGCGGTCTGGGTTATCGTGCCACAG
AATTTCTAATG

Figure 5-69

31G6-3 (2.5X)
Immediately Upstream of promoter (factor sigma 70, predicted 1+ start site 1986220) and gene b1904 (orf, function unknown)

Transposon Tn10 Accession # AY528506
Nucleotide Accession # NA
Protein Accession # NA

AAACGACCGGACCG
GATCATATGACAAGATGTGTATCCACCTTAACTTAATGATTTTTACCAAAATCATTAGGGGATTCATCAG
TGCCNGGCGTNTTTNCCGGCCATTGNCNCAGCACTGNNACGCGTAAAATAGNGCTTTCTCTTACTC
TTCTGGCTGGACCATGAGACTTCTGATTCTGACTCTTTCATTAATATCCCCCCCCCCCG

Figure 5-70

32A4-2 (14X)
Between ptrB & yebE (complement) - ptrB gene - protease II; yebE gene -unknown function

Transposon Tn10 Accession # AY528506
Nucleotide Accession # NA
Protein Accession # NA

NGANNATACGNCCGATCCGG
GATCATATGACAAGATGTGTATCCCCTTAACTTAATGATTTTTACCAAAATCATTAGGGGATTCATCAG
GTTGAAACATCTTATAAGGGGTGGCAAAACTCACCGGGGATGCAAGCGAAACAGGGGAGTCATTG
CTTAGATGATGACAGGTAATGGCGCGGATATCGAATGTTATGCAANCAGANAANANCAGNCTGTT
CAAATGGCTGTGCGATTCTGGATAGCCCGAAATAGTCAACTTCAGGCTATCCAGAGAGCGGAATT
ATTCCGCCAAAGTGCGTTTTTGCTGTTCGAGATCGCGTTCAATGCCGTCACGAACATCCTGGGGGA
TTTTCAGCGCGTCACCCAGTGCATTCAGGTAACTGCGTTCCATAAAATGGTCAATATCAATAGCCG
CGNNACTAATNNACNCGNGGCCNAGCGCCTCTTC

Figure 5-71

35C6-2 (6.5X)
hscA gene (complement)– factor, chaperone; product is heat shock protein chaperone, member Hsp70 protein family

Transposon Tn10 Accession # AY528506
Nucleotide Accession # AE000339
Protein Accession # AAC75579

CGNCCGGATCCGG
GATCATATGACAAGATGTGTATCCACCTTAACTTAATGATTTTTACCAAAATCATTAGGGGATTCATCAG
TGCCGACGGTCTTTTGAGCGTGACGGCGATGGAGAAATCCACCGGCGTTGAGGCGTCTATTCAGGT
CAAACCGTCTTACGGTCTGACCGATAGCGAAATCGCTTCGATGATCAAAGACTCAATGAGCTATGC
CGAGCAGGACGTAAAAGCCCGAATGCTGGCAGAACAAAAAGTAGAAGCGGCGCGTGTGCTGGAA
AGTCTGCACGGCGCGCTGGCTGCTGATGCCGCGCTGTTAAGCGCCGCAGAACGTCAGGTCATTGAC
GATGCTGCCGCTCACCTGAGTGAAGTGGCGCANGGCGATGATGTTGACGCCATCGAACAAGCGAT
TAAAAACGTAGACAAACAAACCCAGGATATCNCCCNNNNCNGTACTAGTCGACGCGTGG

Figure 5-72

37B5-2 (11X)
yedK gene - hypothetical protein, function unknown

Transposon Tn10 Accession # AY528506
Nucleotide Accession # AE000285
Protein Accession # AAC74998

NGAAAAACGTCCGGATCCGG
GATCATATGACAAGATGTGTATCCACCTTAACTTAATGATTTTTACCAAAATCATTAGGGGATTCATCAG
CTCCGCGCCCTGGTTTTTAACATTACCCACCGCGCGCGATATCNNNNNNNNNNGTACTAGTCGACG
CGTGGGCCAANTANNNNNNCNNNNTNNNNNNNTNNNNNNCGNNTNNNGNNNNNCNC

Figure 5-73

41G10-2 (10X)
leuO gene - putative reg of AA biosynthesis (leucine) - Same clone as 14B7-4

Transposon Tn10 Accession # AY528506
Nucleotide Accession # AE000118
Protein Accession # AAC73187

AAAAACCGTTACCGGATCCGG
GATCATATGACAAGATGTGTATCCACCTTAACTTAATGATTTTTACCAAAATCATTAGGGGATTCATCAG
AGTTAAGTGTGACAGTGGAGTTAAGTATGCCAGAGGTACAAACAGATCATCCAGAGACGGCGGAG
TTAAGCAAACCACAGCTACGCATGGTCGATCTCAACTTATTAACCGTTTTCGATGCCGTGATGCAG
GAGCAAAACATTACTCGTGCCGCTCATGTTCTGGGAATATCCCCCCCNNCNGTACTAGTCGACGCN
GN

Figure 5-74

41B10-5 (9X)
leuO gene – same as as 14B7-4

Transposon Tn10 Accession # AY528506
Nucleotide Accession #AE000118
Protein Accession # AAC73187

AAAAACCGTTACCGGATCCGG
GATCATATGACAAGATGTGTATCCACCTTAACTTAATGATTTTTACCAAAATCATTAGGGGATTCATCAG
AGTTAAGTGTGACAGTGGAGTTAAGTATGCCAGAGGTACAAACAGATCATCCAGAGACGGCGGAG
TTAAGCAAACCACAGCTACGCATGGTCGATCTCAACTTATTAACCGTTTTCGATGCCGTGATGCAG
GAGCAAAACATTACTCGTGCCGCTCATGTTCTGGGAATATCCCCCCC

Figure 5-75

44C2-1 (`10X)
ycdS gene (complement) - same clone as 31A4-4

Transposon Tn10 Accession # AY528506
Nucleotide Accession #AE000204
Protein Accession # AAC74109

CNCGCCGGACATCCGGATCCGG
GATCATATGACAAGATGTGTATCCACCTTAACTTAATGATTTTTACCAAAATCATTAGGGGATTCATCAG
GTGACAGTTAGCGCGCCCGGATAATTTTCACTCTCCAGGTGGCTGTAAAAGAGATCCGCAAGTTCT
TCATCGGATAAATCCGGGGCAATGGTCTCCTTGTGATAAAAGAGCTCGGTCATTATTGACTGTGCT
TTTTTCGGCTGATGATCTTTGAGATAAGCCGATGCAACCCAATATTGCCCCCAGGGCGGAATAATT
TGCCCCGTCTTTTTTAATCGCTGATAGTGAGAAATAACGTCTTTATAACGATCGCGAGTTAATAAC
GCGCCAAGATGATCAACCTGAATACGCTGGTACTGGGCAGTGCGGTCT

Figure 5-76

46E5-5 (10X)
ycdQ gene (complement) - putative enzyme homologous to IcaA in Staphylococcus

Transposon Tn10 Accession # AY528506
Nucleotide Accession # AE000204
Protein Accession # AAC74109

AAAAACCGTTACCGGATCCGG
GATCATATGACAAGATGTGTATCCACCTTAACTTAATGATTTTTACCAAAATCATTAGGGGATTCATCAG
GAGCTGGNGCGTTTTCTCCCCACGGCCAGTGGCGTTCACNATAGACCCAGAAATAGACGCCGNCNACAATN
CACATAATGGACATAAAAAACGGCCAGAAGAAAACGAACCTNATCATCAGTTCACCGAGTGAAAGTACGC
TACGCATAGGGGTATGCATAACACCAGACATAATATAAAAAACGATACGATGCGATTAA

Figure 5-77

48A4-5 (20X)
trs5_11 (complement) - IS,phage, Tn; transposon related functions, IS5 transposase

Transposon Tn10 Accession # AY528506
Nucleotide Accession # AE000427
Protein Accession # AAC76530

GAGATACGNCCGGATCCGG
GATCATATGACAAGATGTGTATCCACCTTAACTTAATGATTTTTACCAAAATCATTAGGGGATTCATCAG
TGCTCCACCCTGGCCCGGATGCTGGCTTTCATGTATTCGATGTTGATGGCCGTTTTGTTCTTGCGTG
GATGCTGTTTCAAGGTTCTTACCTTGCCGGGGCGCTCGGCGATCAGCCAGTCCACATCCACCTCGG
CCAGCTCCTCGCGCTGTGGCGCCCCTTGGTAGCCGGCATCGGCTGAGACAAATTGCTCCTCTCCAT
GCAGCAGATTACCCAGCTGATTGAGGTCATGCTCGTTGGCCGCGGTGGTGACCAGGCTGTGGGTCA
GGCCACTCTTGGCATCGACACCAATGTGGGCCTTCATGCCAAAGTG

Figure 5-78

49C2-1 (9X)
ycdS gene - (complement), putative outer membrane protein, not classified

Transposon Tn10 Accession # AY528506
Nucleotide Accession # AE000204
Protein Accession # AAC74109

CGNCCGATCCGG
GATCATATGACAAGATGTGTATCCACCTTAACTTAATGATTTTTACCAAAATCATTAGGGGATTCATCAG
GATGAATTACGGGCGATGACAGAGTCATTACCTGAAAATGCATCTACGCAACAATATCCCACNNA
NTNGTACTAGNCGACGCGTGGCCATCAACTTGCTGCCGCGATTGACGATGCCAATTTAACGCCAGA
TATTCGCGCTGATATTNCTANNCGACGNGCNGGNNGACGCGTGGCCAANGCNNNNCNTNNNCTNN
NAANNNTGNNCNGNNCNCTGGCTGNTGTCCNNNCTGNNANCGCCNCANAACNTCNTGNCNTNNN
NNANGCTGNCGTCCCTTANNGAAGNGGCCNNGGNNAATNATGTNNACNCCNTNNCCAANCGNTTN
NNNACTNNACNANCNACCCNNGATNTC

Figure 5-79

49G12-3 (20X)
ycdS gene (complement) - putative outer membrane protein

Transposon Tn10 Accession # AY528506
Nucleotide Accession #AE000204
Protein Accession # AAC74109

CACGGATCCGG
GATATATGACAAGATGTGTATCCACCTTAACTTAATGATTTTTACCAAAATCATTAGGGGATTCATCAG
CGTTAAATTGGCATCGTCAATCGCGGCAGCAAGTTGATTATTACGTAATGCCTGCACGTATTCTGT
GGGATATCCNNCCCNCCCGTACTAGTCGACGCGTGGCCATGNNATNNNCCGNNATTCATNCTGAT
GACNCCCCGNCAGTTTATANATATNNNNNNNNNNGTNCT

Figure 5-80

51A10-4 (2X)
modC gene – ATP-binding component of molybdate transport; Transport of small molecules: Anions

Transposon Tn10 Accession # AY528506
Nucleotide Accession # AE000179
Protein Accession # AAC73852

AACGCACCGGATCCGG
GATCATTGACAAGATGTGTATCCACCTTAACTTAATGATTTTTACCAAAATCATTAGGGGATTCATCAG
ACTGACGCGCCCGCAAAAAGGGCGGATTGTCCTCAATGGGCGGGTACTAAATGATGCCGAAAAAGGTATC
TGCCTTNCCGTACTAGTCGACGCGTGGCCACNNNTTCATTCNCCNCTANCTCNNAAGTNNNCCNACTCCGN
GNNCNACCNNCCNNNCCCCNTNGCAGNCNTGTNCNCNNACNNCGGCNACCCNNNGANNNCGNCTCCNCCC
GCCCCTNTCNNCACCTNNNNANGGCNTACCNGCCCCTCNNGCTCNGTTACCTTNNTNNNTNNCCGNCCCCN
CTCANANNCNCCNTNACNNGNCNNNCNATNCNTCGCNNNNNNAGTANNCCCNCNTCCCCCCACNCNCNNN
CCGTNTTNNCNCTTNAGANCT

Figure 5-81

56C11-1 (5.5X)
modC gene – Same clone as 51A1-4

Transposon Tn10 Accession # AY528506
Nucleotide Accession # AE000179
Protein Accession # AAC73852

AACGNACCGGATCCGG
GATCATATGACAAGATGTGTATCCACCTTAACTTAATGATTTTTACCAAAATCATTAGGGGATTCATCAG
ACTGACGCGCCCGCAAAAAGGGCGGATTGTCCTCAATGGGCGGGTACTAAATGATGCCGAAAANGGTNTC
TTGCCTGNCCCGTACTANTCGACGCGTGGCCAACNAACCTNCTTCNTANNNTCGCNNTTCCCCCTTCNGCNC
NTCNNCCACTCCCNGCTGCTCCTNCNNCCTTCCNCGCNCCNTACCNTCGTNNCCTTANTCCACCTGCNNCTA
TCCCNCGGCCCGNCCTCCCGNCCCCCCNCTNCAANTNGTTCANGNACNGNCCNCCCTCGCCCNAGCGCTNC
CNGNGCCAGNNNCTNTTCATNTCCCTCCCNGATCCANTCNCNNCCNTTNCNCTCTNACNNNCCNGTCNCTN
NCCCCCTNNTTAN

Figure 5-82

62C9-2 (20X)
yecK gene (complement) - putative enzyme (cytochrome C type); not classified ,product homologous to TorC cytochrome of TorCAD resp. system

Transposon Tn10 Accession # AY528506
Nucleotide Accession # AE000281
Protein Accession # AAC74943

CNCGACCGG
GATATATGACAAGATGTGTATCCACCTTAACTTAATGATTTTTACCAAAATCATTAGGGGATTCATCAG
GGTTTCGCTGTCCTTTTGTGCTTTGTTATGCATTTTCTGCGCAGATTCACTTTGCGAGGCAATATCC
ATGGCATCAAAANAATGGCAACTACGGCACGTTGCAGAGTCAGTGGCTTTTAATTCTTTCCATACT
GTTTCGGCCATTTCCTGGCGATGAGCTTCGAACTTATCGTCACTGTCTATTTTGCCGCTAACAAATT
CATGATAAATATCTTTAGATGC

Figure 5-83

63E2-3 (2X)
between genes clpP and clpX – clpP: enzyme; degradation of proteins; ATP-depentent proteolytic subunit of clpA-clpP serine protease, heat shock protein F21.5. clpX: enzyme; degradation of proteins, ATP-dependent component of serine protease, chaperone.
Transposon Tn10 Accession # AY528506
Nucleotide Accession # NA
Protein Accession # NA

AAACNNCCGGATCCGG
GATCATATGACAAGATGTGTATCCACCTTAACTTAATGATTTTTACCAAAATCATTAGGGGATTCATCAN
GGTTTTGACCCATGACAGATAAACGCAAAGATGGCTCATGCANATTGCTGTATTGCTCTTTTTGCGGCAAAA
GCCNNCATGAAGTGCGCCAGCTGANNAGCCGGNCCATCCCTNTATATCNNCCNNCCCTGTACCTNGNCGGN
CNCGTGGNCNNNCTCCTNTCNTTNNCNTCTCCCCNNTCTNNNNCCCCTCTNNCGCGGNCCCNCTGANNCGC
CTCNCTTCTTNTACCTCCNCGNGCCTCTACCNCTCGNNCCTCNCCCCCCACCTCCTTATTCCNCCTCCNTCNT
NTCCNTCTCCACCTNTCCTTTCCNACCGCNNCATNNNACGTCTCNTTCCCTNNNNCCACNNNTNATCCTTCN
GCNCCCCTCNGNGCGAANCNTCNCTNNNCTANCGGCNCGNTGNNCNTGCNNCNCANTNANCNCNCNCTNA
TTGAGTGCGNGT

Figure 5-84

66E10-1 (12X)
ycdS gene (complement) - putative outer membrane protein, same as above

Transposon Tn10 Accession # AY528506
Nucleotide Accession #AE000204
Protein Accession # AAC74109

CNCGATCCGG
GATATTGACAAGATGTGTATCCACCTTAACTTAATGATTTTTACCAAAATCATTAGGGGATTCATCAG
GTGACGACATCCGTGCCATAATGTTTTTGCCAGGAGGCACCAACACCTGCGCTGAATATTTGCTCCCAGCTA
TTTTCATAGCTTCGCCATAACAAATGGCTTGCCTCAAATGCCGGAACAATATCNNNCNNNNNNGTACTAGT
CGACGCGTGCCA

Figure 5-85

68E11-2 (2.5X)
glnE gene (complement) – enzymes, translation and modification; Adenylylating enzyme for glutamine synthetase

Transposon Tn10 Accession # AY528506
Nucleotide Accession # AE000387
Protein Accession # AAC76089

AAACCCACCGGATCCGG
GATCATATGACAAGATGTGTATCCACCTTAACTTAATGATTTTTACCAAAATCATTAGGGGATTCATCAG
AGTTTTATCTGCGTCTGGCGCAACGCATTATGCATCTGTTCAGTACGCGTACCTCTTCCGGCATTTT
GTATGAAGTGGATGCTCGACTGCGTCCGTCCGGGGCGGCGGGAATGCTGGTGACATCCGCAGAAG
CATTTGCCGATTATCAGAAAAACGAGGCCTGGACGTGGGAACATCAGGCGCTGGTGCGTGCGCGT
GTAGTGTACGGCGATCCGCAGCTCACCGCGCACTTTGACGCAGTGCGTCGCGAGATTATGACGCTG
CCGCGTGAAGGTAAAACTCTGCAAACGGAAGTGCGGGAAATGCGCGAGAAAATGCGCGCTCATCT
CGGCAATAAACATCGCGATCGCTTTGATATCAAAGCTGATGAAGGGGGAATTACCGATATCGAAT
TTATTACCCAAT

Figure 5-86

68A3-1 (>24X)
wcaI gene (complement) - putative enzyme, colanic acid biosynthesis

Transposon Tn10 Accession # AY528506
Nucleotide Accession # NC_000913
Protein Accession # NP_416554

GNCNNCTAAAAACNTTACCGGATCCGG
GATCATATGACAAGATGTGTATCCACCTTAACTTAATGATTTTTACCAAAATCATTAGGGGATTCATCAN
GGCCGNNANGGTGTGGCGCTGCCCGCTGTATGTGCCAAAACAGCCGAGCACCCTGAAACGCCTGT
TGCATCTGGGCAGTTTTGCCGTCAGCAGTTTCTTTCCGCTGATGGCGCAACGTCGCTGGAAGCCGG
ATCGCATTATTGGCGTGGTGCCAACGCTGTTTTGCGCGCCGGGAATGCGCCTGCTGGCGAAACTCT
CTGGTGCGCGTACCGTGCTGCATATTCAGGATTACGAAGTGGACGCCATGCTGGGGCTGGGCCTTG
CCGGAAAAGGCAAAGGCGGCAAAGTGGCACAGCTGGCAACGG

Figure 5-87

73E6-6 (16X)
ycdS gene (complement) – putative outer membrane protein, not classified

Transposon Tn10 Accession # AY528506
Nucleotide Accession #AE000204
Protein Accession # AAC74109

CGNCCGGATCCGG
GATCATATGACAAGATGTGTATCCACCTTAACTTAATGATTTTTACCAAAATCATTAGGGGATTCATCAG
CGCATCTGGTCTTCACCATATTTGATTGTCGATTTCCTACCCAGTCTGTATTACGAACAAAATACAG
AACACGATACCCCATACTACAACCCTATAAAAACGTTCGATATNGTTCCGGCNTGTGCTGCNCGNC
NNGTGGNCTGGCGAAGCTATGAAAATAGCTGGGAGCAAATATTCAGCGCAGGTGTTGGTGCCTCC
TGGCNAAAACATTATGGCACGGATGTCGTCACCCAACTCGGCTACGGGCAACGCATTAGTTGGAA
TGACGTGATTGATGCTGGCGCAACGCTACGCTGGGAAAAACGACCTTATGACGGTGACAGAGAAC
ACAACTTATACGTTGAATTCGATATGACATTCAGATTTTAAGGATAAATATGTTACGTAATGGAAA
TAAATA

Figure 5-88

73E9-1 (12X)
ycdS gene (complement) - putative outer membrane protein, not classified

Transposon Tn10 Accession # AY528506
Nucleotide Accession #AE000204
Protein Accession # AAC74109

ACGNCGGATCCGG
GATCATATGACAAGATGTGTATCCACCTTAACTTAATGATTTTTACCAAAATCATTAGGGGATTCATCAG
CACCGTACTTACGCCGCTCATTTTGATACCANCGAACATAAGCCTGAGCACTGTTGCCTGTAACACCATTTT
TCATTGCCCGTAATGGAACGCGGTGAGAGAGGCGTTCCAGTTGCGAACCAATACGCCAGTTATCATTAAAA
TCATATCNGCCNGNCCNGTACTAGTCGACGCGTGGCCANAAATTGAAAACTGGTTTGCCANAATTNTCTNG
ATCNCCTAAAAAGCTATNACTGGACNCGNTATNATGGNTNTGNNTTATCTGGNANGGGGNNNCANAAAAA
TNCGNTGCCAATGGNTNATNCAATTGNCCATNAAATTAAAAACATCCCTTANGNTNAAAGACAAATNNATT
TTNTAATTCANGGGCNA

Figure 5-89

73F2-1 (12X)
ycdS gene (complement) - putative outer membrane protein

Transposon Tn10 Accession # AY528506
Nucleotide Accession #AE000204
Protein Accession # AAC74109

NNGNAAACCAGCCGGACNTCCCGGATCCGG
GATCATATGACNAGATGTGTATCCACCTTAACTTAATGATTTTTACCAAAATCATTANGGGATTCATCAG
NCAGATGCGTTCCTGACCCTCAAGNGAGACTTCATGACGCTGGTTACTGTCGGAAAAATCAGTGA
AAGCCCAGGANACACCGTACTTACGCCGCTCATTTTGATACCAGCGAACATAAGCCTGAGCACTGT
TGCCTGTAACACCATTTTTCATTGCCCGTAATGGAACGCGGTGAGAGAGGCGTTCCAGTTGCGAAC
CAATACGCCAGNTATCATTAAAATCATATCNNCCNGAAGAGGACTAGTCNACGCGTGGCCANNAC
ANCCNCACTNNTNAACNTGNGGCTACNANTNTACCNGCCCANNAGNNTTACNTNANTTNCGCNCN
CCTNCCANTCNCNCCCNNANGTNNNCNNAANCTNNANNCTN

Figure 5-90

75E11-5 (1.5X)
moaC gene - enzyme, biosynthesis of cofactors, carriers: molybdopterin; molybdoproterin biosynthesis, protein C

Transposon Tn10 Accession # AY528506
Nucleotide Accession # AE000181
Protein Accession # AAC73870

NNAANATACGGTTCCGGNTCGG
GATCATATGACAAGATGTGTATCCACCTTAACTTAATGATTTTTACCAAAATCATTAGGGGATTCATCAG
ATGGAAGCATTAACCGCGGCCTCCGTGGCGGCGCTGACCATTTATGACATGTGCAAAGCGGTGCA
AAAAGATATCNCNNNCCNNNGTACTAGTCGACGCGTGGCCAAANATCNGGGNTCTCNNNNTGCTN
GCTNCNAATCNANTGNACCCNCTNAACCCNTTCNAGCTAAACATNTNNATNTGNAACNNATAAAC
NCAGGACGNCACTATNGNGTNNACNT

Figure 5-91

84A10-6 (11X)
ycdR gene - orf, unknown function, product homologous to IcaB in S. aureus

Transposon Tn10 Accession # AY528506
Nucleotide Accession # AE000204
Protein Accession # AAC74108

CGNNGANACGNCCGAATCCG
GATANTANACAAGATGTGTATCCCCTTAACTTAATGATTTTTACCAAAATCATTAGGGGATTCATCAG
GGCTTTAGCGGGAGTCTGAGCGAAATTCGACAAAACCCGGAGCAATTTAAACAGTGGGCCCGCTT
TAAAAGTCGTGCGTTAACTGACTTCACTTTAGAACTTAGTGCGCGCGTAAAAGCCATTCGCGGTCC
ACATATTAAAACTGCACGAAATATTTTTGCACTTCCGGTAATACAACCTGAAAGTGAAGCCTGGTT
TGCACAGAATTATGCTGATTTCCTAAAAAGCTATGACTGGACCGCTATTATGGCTATGCCTTATCT
GGAAGGTGTCGCAGAAAAATCGGCTGACCAATGGTTAATACAATTGA

Figure 5-92

86E7-6 (10X)
ycdQ gene (complement) - orf, unknown, putative enzyme homologeous to IcaA in Staph

Transposon Tn10 Accession # AY528506
Nucleotide Accession #AE000204
Protein Accession # AAC74109

NACGGATCCGG
GATATATGACAAGATGTGTATCCACCTTAACTTAATGATTTTTACCAAAATCATTAGGGGATTCATCAG
TATCTGGTGTGCATTGATGGCGATGCGTTATTAGACCGCGATGCGGCGGCATATATTGTGGAACCG
ATGTTGTACAACCCGCGTGTGGGTGCCGTAACCGGTAATCCTCGTATTCGAACACGTTCTACCCTG
GTGGGTAAAATTCAGGTTGGCGAGTATTCCTCAATTATTGGTTTGATCAAGCGAACCCAGCGTATC
TATGGAAACGTATTTACCGTTT

Figure 5-93

86F11-6 (11X)
ycdQ gene (complement) - same clone as 86E7-6

Transposon Tn10 Accession # AY528506
Nucleotide Accession #AE000204
Protein Accession # AAC74109

NCGATCCGG
GATCATTGACAAGATGTGTATCCACCTTAACTTAATGATTTTTACCAAAATCATTAGGGGATTCATCAG
TATCTGGTGTGCATTGATGGCGATGCGTTATTAGACCGCGATGCGGCGGCATATATTGTGGAACCG
ATGTTGTACAACCCGCGTGTGGGTGCCGTAACCGGTAATCCTCGTATTCGAACACGTTCTACCCTG
GTGGGTAAAATTCAGGTTGGCGAGTATTCCTCAATTATTGGTTTGATCAAGCGAACCCAGCGTATC
TATGGAAACGTATTTACCGTTTCC

Figure 5-94

87C5-1 (1.5X)
aroD gene – amino acid biosynthesis: Chorismate, enzyme; product is 3-dehydroguinate dehydratase

Transposon Tn10 Accession # AY528506
Nucleotide Accession # AE000264
Protein Accession # AAC74763

AAACNTACCGGATCCGG
GATCATATGACAAGATGTGTATCCACCTTAACTTAATGATTTTTACCAAAATCATTAGGGGATTCATCAG
CGGCGAGCAGGCGATTTCCACCGAGGCTTATATCCCCCCCNNCCGTACTAGTCGACGCGTGGCCAANTATC
NNGATNNCCCCGCCTGTCANNCNANCCCCCCCTGCGNCCCCTCNTCCNACTCNANCNTAGACCNGCCNCTN
NTNNNNCANCTCNCGGCGCNTGTNCCAACCTGCNCCNCCCCGTCCTGCCNACNCTCTCCACGNCNCNNCCN
NTTNCCCNGCCCTGCCNNCTCTCCCCCCCNCCNCCACNCTCNGNCCCTCAGNCNCNGTCCCGCTCGGTNCNC
CNACNCNNCNCNNNNAGCTCTCCNGTTACCTCACCGATGNTCNCCCCCCTCGNGNGCNCACCCCNNAGCAG
CCNCNTNNNC

Figure 5-95

89E11-5 (8X)
leuO gene – same clone as 14B7-4

Transposon Tn10 Accession # AY528506
Nucleotide Accession # AE000118
Protein Accession # AAC73187

AACGGNCCGGATCCGG
GATCATATGACAAGATGTGTATCCACCTTAACTTAATGATTTTTACCAAAATCATTAGGGGATTCATCAG
AGNTAAGCGTGACAGTGNTANTNNNCTACNGCCANAGGTACAAACAANTTCATNCATNNGCCGCNGAAGA
TTTCCTTNTNNNAGCNNNCAGCCNNGNNTNTTNNNCANTNTCCTAACCCNTNNCNCNTGGTNGTNANNNCA
NGTTCATNNNNCATTNANTGNNTNTNTCGANTNCGCNTCNC

Figure 5-96

90A11-6 (3X)
rnpB gene (complement) - Enzyme; Degradation of RNA/RNase P, RNA component; M1 RNA; processes tRNA,4.5S RNA

Transposon Tn10 Accession # AY528506
Nucleotide Accession # P06277
Protein Accession # P06277

GNAAAGCCCGCCGGACATCCCGGATCCGG
GATCATATGACAAGATGTGTATCCACCTTAACTTAATGATTTTTACCAAAATCATTAGGGGATTCATCAG
AGCCGGAAGTNAACGCGGNGCTGGAGAAGATGAAAACCTTCTCANAAGCGATTATTTCCGGTGAG
TGGAAAGGNNATACCGGCNAAGCAATCACTGACGTAGTGAATATCNCNCNCCCCNGTACTAGTCG
ACGCGTGGCCACANNNNNNNNNNNNNNCNNNNNNC

Figure 5-97

90E7-1 (2X)
aroD gene – amino acid biosynthesis, Chorismate; 3-dehydroquinate dehydratase

Transposon Tn10 Accession # AY528506
Nucleotide Accession # AE000264
Protein Accession # AAC74763

ACGACCGGATCCGG
GATCATATGACAAGATGTGTATCCACCTTAACTTAATGATTTTTACCAAAATCATTAGGGGATTCATCAG
TGCTCGCCGCCTTCTTTGGCACTGCGGAAGGTAAACAGCAGCNGTTTTTCTGGCATGGACTCACGGAGAATT
TTTGCTGCCGCCATGACAGACTCCACATTGGAGNGGTANGCATNCTGGNCCACACNCCATTCCANANTATC
NNCTTTNNCTGCNACTANTNANNNCTCGNANTNTTNCNTCNCNNNNCNCNCANTTCCTCNNCCTTNNACNN
NCGNGNNNNTTGTTGAANNNTTNNNACANCNCANNTTCNCCCCNCNTCTNNTANATNNGNCCCNNGCCTN
NNAGTNNTANTNCNNTTTNNTC

Figure 5-98

91F9-6 (2X)
b2531 gene – orf, function unknown; hypothetical protein

Transposon Tn10 Accession # AY528506
Nucleotide Accession # NC_000913
Protein Accession # NP_417026

CGTACCGGATCCGG
GATCATATGACAAGATGTGTATCCACCTTAACTTAATGATTTTTACCAAAATCATTAGGGGATTCATCAN
GGGCCCGGTACCGTTGGCTGATATTTCCGAACGTCAGGGAATTTCCCTTTCTTATCTGGAACAACTGTTTTC
CCGTCTGCGTAAAAATGGTCTGGTTTCCAGCGTACGTGGACCAGGCGGTGGTTATCTGTTAGGCAAAGATG
CCAGCAGCATCGCCGTTGGCGAAGTAATTAGCGCCGTTGACGAATCTGTAGATGCCACCCGTTGTCAGGGT
AAAGGCGGCTGCCAGGGCGGCGATAAATGCCTGACCCACGCGCTGTGGCGTGATTTGAGCGACCGTCTCAC
CGGTTTTCTCAACAACATTACTT

Figure 5-99

93E3-6 (12X)
ycdR gene (complement)– orf, function unknown; product homologous to IcaB in S. aureus

Transposon Tn10 Accession # AY528506
Nucleotide Accession # AE000204
Protein Accession # AAC74108

CGNCCGGATCCGG
GATCATATGACAAGATGTGTATCCACCTTAACTTAATGATTTTTACCAAAATCATTAGGGGATTCATCAG
GGCTTTAGCGGGAGTCTGAGCGAAATTCGACAAAACCCGGAGCAATTTAAACAGTGGGCCCGCTT
TAAAAGTCGTGCGTTAACTGACTTCACTTTAGAACTTAGTGCGCGCGTAAAAGCCATTCGCGGTCC
ACATATTAAAACTGCACGAAATATTTTTGCACTTCCGGTAATACAACCTGAAAGTGAAGCCTGGTT
TGCACAGAATTATGCTGATTTCCTAAAAAGCTATGACTGGACCGCTATTATGGCTATGCCTTATCT
GGAAGGTGTCGCAGAAAAATCGGCTGACCAATGGTTAATACAATTGACCAATCAAATTAAAAACA
TCCCTCAGGCTAAAGACAAATCTATTTTAGAATTACAGGC

Figure 5-100

96B10-1 (11X)
nhaR - regulator, transport of sm molecules - cations; encodes a positive regulator for nhaA(a Na/H antiporter) stimulates transcription of osm-c

Transposon Tn10 Accession # AY528506
Nucleotide Accession # AE000112
Protein Accession # AAC73131

NCAACGTNCCGGATCCGG
GATCATATGACAAGATGTGTATCCCCTTAACTTAATGATTTTTACCAAAATCATTAGGGGATTCATCAG
GTTTATGCTGACTTAATTGCTCCAGCAGCATTTCGTGGGTGGATTCGAAGCAGCGAAGATGAATGG
GCTCGCCTTCTACCACTGCGGCGTTAAGTACGCTACTGACCAGGCGTTTGGAAAGTGCATCAGCCA
CGCCAACGTCAAACAATAAATTGGATTCTTTGCGATAGTTCACAATATCCNNCNNNNCCGTACTAG
TCGACGCGTGGCCAN

Figure 5-101

102G9-5 (5X)
leuO gene – Same clone as 14B7-4

Transposon Tn10 Accession # AY528506
Nucleotide Accession # AE000118
Protein Accession # AAC73187

AAACNCACCGGATCCGG
GATCATATGACAAGATGTGTATCCACCTTAACTTAATGATTTTTACCAAAATCATTAGGGGATTCATCAG
AGTTAAGTGTGACAAGTGGAGTTAAGTATGCCANAGGTACAAACAGATCATNCAGAGACGGNGG
AGTTAAGCAAACCACAGCTACAGCATGGTCGATCTCAACTTATTAACCGTTTTCGATGCCGTGATG
CAGGANCAAAACATTACTCGTGCCGCTCATGTTCTGGGAATATCNCNNNNGCNNGNACTAGTTCG
ACGCGTGGCCNCATANNATGTNTCNNNTTCNNNNCTCTTCNNTTGCTTCCCTTNCCCCTCTTCCNGC
CCCCCANNNCGTCTNNTNTNNATCNNGNNCTTNNCNTACGACTN

Figure 5-102

106B2-6 (5X)
leuO gene – same clone as 14B7-4

Transposon Tn10 Accession # AY528506
Nucleotide Accession # AE000118
Protein Accession # AAC73187

AAACCCNTNGGATCCNG
CATCATATGACAAGANGTTGTATCCACCTTAACTTAATGATTNTTACCAAANTCATTAGGGGATTCATCAN
AGTTAAGTGTGACAGTGGAGTTAAGTATGCCAGAGGTACAAACAGATCATCCAGAGACGGTGGAGTTAAG
CAAACCACAGCTACNGCATGGTCGATCTCAACTTNTTAACCGTTNTCGATGCCGTGATGCAGGAGCAAAAC
ATTACTNCGTGCCGNTCATGTTCTGGGAATATCCCNNGGNNACGTNCTAGTCNANGCGTGGCCAANNGNTN
NGGNNNCTNANTCACAGNANCTTTANNNGTN

Figure 5-103

109B4-4 (2X)
Between two protein binding sites (complement) - 1)central position to predicted promoter: -0.5/LexA predicted site and 2)documented lrP site/ central position to leuABCD promoter:- 156.5

Transposon Tn10 Accession # AY528506
Nucleotide Accession # NA
Protein Accession # NA

AGCNCGCCGGACNTCCCGGATCGG
GATCATATGACAAGATGTGTATCCACCTTAACTTAATGATTTTTACCAAAATCATTAGGGGATTCATCAG
TCGGTAGTTAAGCAGAAATTAATATCGCTTACTTTAACCACCGCAGCACAATTAGCTAATTTTACG
GATGCAGAACTCACGCTGGCGGGACGTTTTTATTGCGTCAGGGTTGACATCCGTTTTTGTATCCAG
TAACTCTAAAAGCATATCGCCCCCNCCNGTACTAGTCGACGCGTGGCCANAACNCGNNNNTCCAN
TNTNNCC

Figure 5-104

110G8-2 (9X)
ycdS gene (complement) - putative outer membrane protein

Transposon Tn10 Accession # AY528506
Nucleotide Accession # AE000204
Protein Accession # AAC74109

GNAANGNAAAACNCGCCGGACATCCCGGATCCGG
GATCATATGACAAGATGTGTATCCACCTTAACTTAATGATTTTTACCAAAATCATTAGGGGATTCATCAG
NACNGCNNATTGNNCCCACGGNGGANTAANTNGCCCCNGNTTGNNNTCTCGCTGNTAANGANAAA
TAACGTCTTTATAACGANCGCGAGTNAATAACGCGCCAAGATGATCAACCTGAATACNCTGGTAC
TGGGCAGTGCGGTCTGGGTTATCGTGCCACAGAATTTCTAATGCAGCGTATTGGGCGAGGGCGCG
ATCGGCAATGGCATAACGNTCACTTTCACTGCGCGTAGGCATAAACGACAGTCTGACCAGTTCGGC
ATGAATATCAGNNNTTGNTGNACTAGNCNACGCGTGGNCAAAACAT

Figure 5-105

115C12-5 (16X)
ycdR gene (complement) – orf unknown function; product homologous to IcaB in S. aureus

Transposon Tn10 Accession # AY528506
Nucleotide Accession # AE000204
Protein Accession # AAC74108

CGNCCGGATCCGG
GATCATATGACAAGATGTGTATCCACCTTAACTTAATGATTTTTACCAAAATCATTAGGGGATTCATCAG
AGCTTAATACCGGCATCCACGCATAGATGTTTACACCTGAGCGGGTACGTAATTGCCAGGCAACCC
GACTAAAAATATCTGCTTTCATTGGNCTNANACAANCGNGGANCCAGACCTCTTTGACCAGCCCAT
CACCATCGGGATCAGCAAATGCCTGCAAATACACGGTTGATATTTGCATATCTTTCCCCCNCGTAC
TAGTCGACGCGTGGCCACATTACTTNTANTNTANNANTGGATCCNANTNANNCGGNTNTANCTNG
CCTTGNANGGGNGNNANNATTATCNNCTGCCNNCGACNAANT

Figure 5-106

123F5-6 (4X)
modA gene - transport, small molecules: anions; molybdate-binding periplasmic protein; permease

Transposon Tn10 Accession # AY528506
Nucleotide Accession # AE000179
Protein Accession # AAC73850

TTTNNGAAACACGCCGNACATCCCGGATCCGG
GATCATATGACAAGATGTGTATCCACCTTAACTTAATGATTTTTACCAAAAATCATTAGGGGATTCATCAG
TGGATTATGCGGTTGATAAAAAAGCGATCGATACAGCTACGCGTCAGACACTGCTCGGCAATAGC
CTGGTCGTTGTAGCACCGAAAGCCAGCGTGCAGAAAGATTTCACCATCGACAGCAAAACCAACTG
GACTTCACTGCTGAATGGCGGTCGCCTGGCGGTTGGCGATCCGGAACATGTTCCCGCTGGCATTTA
TGCAAAAGAAGCACTGCNAAAACTGGGCGCATGGGATACNCTCNCTCCGAAAATGGNCCCNCNTA
AGNTGNTCCTAGGGGNNCNNNCGCNGGTCACCACNTAATCGAACCN

Figure 5-107

125A7-1 (2.5X)
rbsK gene - enzyme, degradation of small molecules: carbon compounds; ribokinase

Transposon Tn10 Accession # AY528506
Nucleotide Accession # AE000452
Protein Accession # AAC76775

GCAAAAACGANNCGGCCAAG
GATCATATGACAAGATGTGTATCCACCTTAACTTAATGATTTTTACCAAAAATCATTAGGGGATTCATCAG
GAAAGGGCAGCNTTANCGCCGGCATGAATACCGATGACATTCTCACCTTCGCCATTAACAAAAAT
CANCGCCACACCTGTTGATTCGCCTTTGATCTCGCTGACCGGAGTAANATCCCCNTNNNNGNACTA
GTCNACGCGTGGCCATNAANTTCNNNCGACCNTANGACCCNANTCCTGNNNTTAANNCNCGNNTN
CCNTANTTGCNCCANNNN

Figure 5-108

125E4-1 (24X)
insB_4/insA_3/insA_2 genes (complement) - all three have the same probability score and identities,89% - IS,phage,Tn; transposon-related function

Transposon Tn10 Accession # AY528506
Nucleotide Accession # NA
Protein Accession # NA

CACANCCGNACATCNGCGNT
ATNNCTACTNANAATGNCGTGAANTATTCNCNACTGCNTNACACTTACACCGNNTCTCATNCCGGTANGC
ACCACANAAANNTTGAATATGAGGCATGAATGGTNGTTGGANGCCGGGTAACAGCCNTCATTATG
GGNGTTGGCCTCAACACGATTTTCCTCCNTTTAAAAAACTCACGCCGNTACCCTGTAACCTCGCAC
CATACTGGCAGGGCAGCNGACNGATTCGCCTGCGCATGAAATGNANAAACNNTGGGGATNCACCA
GGGNGTAAATCTNGCCAGCGATNNCTGNNTTNNTCTTNTGANANGATNCNGAAAANGGGGGNTGC
NCNCGTNTNCCGGNAAACATCNNTAATAAAACTGGGGCCAAAGTAAAACGTCNGGATATCCAATC
CANNNGTACTANTCGACGCGTGGCCANNACTGNC

Figure 5-109

126C5-4 (7.5X)
leuO gene - same clone as 14B7-4

Transposon Tn10 Accession # AY528506
Nucleotide Accession # AE000118
Protein Accession # AAC73187

NNACGCTNCGGNNCGG
GATCATATGACAAGATGTGTATCCACCTTAACTTAATGATTTTTACCAAAATCATTAGGGGATTCATCAN
AGTTAAGTGTGACAGTGGAGTTAAGTATGCCAGAGGTACAAACAGATCATCCAGAGACGGCGGAG
TTAAGCAAACCACAGTCTACGCATGGTCGATCTCAACTATTAACCGTTTTCGATGCCGTGATGCAG
GAGCAAAACATTACTCGTGCCGCTCATGTTCTGGGAATATCNCCCCNCTNNGTACTAGTCGACGCG
TGGCCANN

Figure 5-110

130E8-4 (24X)
Between yecK and cutC genes (complement) - in a protein binding area with no predicted promoter; TyrR predicted site

Transposon Tn10 Accession # AY528506
Nucleotide Accession # AE000118
Protein Accession # AAC73187

ATNCNCGACCGG
GATCATATGACAAGATGTGTATCCACCTTAACTTAATGATTTTTACCAAAATCATTAGGGGATTCATCAN
NGTCCAGTAATTCAATTANAGGAATCTATGCGNGGGANAAACGGNTGGCNGCTNCNCGCTAANGC
NAANAANTAANCCNCCTNNNNCTANGTATNNNNGGNCNNTNNNANNNCNGNTTTCT

Figure 5-111

130G11(2.5X)
aroD gene – enzyme: amino acid biosynthesis: chorismate; 3-dehydroquinate dehydratase

Transposon Tn10 Accession # AY528506
Nucleotide Accession # AE000264
Protein Accession # AAC74763

ANNCNNCGACCNG
GNTCATATGACAAGATGTGTATCCACCTTAACTTAATGATTTTTACCAAAATCATTAGGGGATTCATCAG
TCNGGCCGANCNGGCNATTTCCACCGAGGCTTATNTCCNCNNNTNTCGNNCTAGNCGNNGCNTGG
CCANGNTTNCGNCCNNCNTNACNCNCTCCATNANTNTNNCCNCTNTCNCNNANTACNGTGCCCGN
GNATNCCCNTCCTCCGTCGGCCCCCNCNNGCTTAGCNGCNNANTGGCCNNNNNNCAANTTANGAC
GATCNGCCNGCCCNNTNAACNGNGTTNGCCATNTNCNTNCNCTNTTATN

Figure 5-112

140B5-1 (9X)
miaA gene – enzyme, Aminoacyl tRNA synthetases, tRNA modification; delta(2)-isopentenylpyrophosphate tRNA-adenosine transferase

Transposon Tn10 Accession # AY528506
Nucleotide Accession # AE000489
Protein Accession # AAC77128

CGNCCGGATCCGG
GATCATATGACAAGATGTGTATCCACCTTAACTTAATGATTTTTACCAAAATCATTAGGGGATTCATCAG
AGGCAAGTCCGTATGCAAATCTCCTCGGGCAAAAAGCGCCCGGACTTCTGCTTCAAAACCTGAAG
CCAACATCTGATGAAAACGCTGCTCAATGCGTTGATGGAGCAGTTCACGGCTCGCCGGGGCGATG
GCGAACTGATGCACCTGATACGGTAGAGCGTCTCCTGACGTTTGCGTCAGTTCCGTTAAAGTTTTA
CCCGAAATGAAAAAAACTTCCAGTGCCCGGGAAAGCCTTTGTGGATCATTTGGATGAATCCTTGCT
GCCGCAACCGGATCTACCTCCTGAAGTTGACGATGCAATGACTCCCAACCTTGCTCTGCCGCCTGT
TGCTCAATTCTGGCCCGTACTTCCGGGTCTGCCGACGGTAGCGGCGACAACCCTTCCAGCAATGCC
TTGAAAT

Figure 5-113

141G2-2 (16X)
yjjQ gene - putative regulator, not classified

Transposon Tn10 Accession # AY528506
Nucleotide Accession # AE000507
Protein Accession # AAC77321

GNCGGATCCGG
TATATATGACAAGATGTGTATCCACCTTAACTTAATGATTTTTACCAAAATCATTAGGGGATTCATCAG
GATGGGGCATCAACCAGATAGCTTCATTGCTTAAGAAAAGTAATAAAACTATCANCGCCCAAAAA
AACAGTGCGATGCGTCGACTGGCAATTCACAGCAACGCTGAAATGTATGCATGGATAAATAGCGC
GCAGGGTGCAAGAGAACTTAACTTGCCTTCTGTTTATGGAGATGCCGCAGAATGGAACACAGCCG
AATTAAGAAGAGAAATGTCGCACTC

Figure 5-114

141G4-6 (18X)
ycdS gene (complement) - putative outer membrane protein; not classified

Transposon Tn10 Accession # AY528506
Nucleotide Accession # AE000204
Protein Accession # AAC74109

NNNAAAGCACGCCGGACATCCGATCCGG
GATCATATGACAAGATGTGTATCCACCTTAACTTAATGATTTTTACCAAAATCATTAGGGGATTCATCAG
ACCCAATATTGCCCCCAGGGCGGAATAATTTGCCCCGTCTTTTTTAATCGCTGATAGTGAGAAATA
ACGTCTTTATAACGATCGCGAGTTATAACGCGCCAAGATGATCAACCTGAATACGCTGGTACTGGG
CAGTGCGGTCTGGGTTATCGTGCCACAGAATTTCTAATGCAGCGTATTGGGCGAGGGCGCGATCGG
CAATGGCATAACGTTCACTTTCACTGCGCGTAGGCATAAACGACAGTCTGACCAGTTCGGCATGAA
TATCANCGCGAATAGTACTAGTCGAC

Figure 5-115

145F10 (3X)
ykgK gene (complement) - putative regulator; not classified

Transposon Tn10 Accession # AY528506
Nucleotide Accession # AE000136
Protein Accession # AAC73397

NNNNGAAGCNCGCCGGACATCCCGGATCCGG
GATCATATGACAAGATGTGTATCCACCTTAACTTAATGATTTTTACCAAAATCATTAGGGGATTCATCAG
TACCACGCCCCTAATATTGCTATTGTAATACCAATAATTTGCTAAGGCCTCTGACTTTCTGGCCGCA
ATCAATACGACCTGTTTCCCCTTTACCGCGGATAACCATTCATTATCACGGTTTATAAATTCAGATA
AAGAATCCGTACTGAGATTGATAAACACGAAATCTTTTCTAATTTTCTCCAACGATAGATAAATTA
ATCTGTCGATATCCCCCNNCNNNGTACTAGTCGACGCGTGGCCA

Figure 5-116

150E3-6 (20X)
ycdP gene (complement) – orf, hypothetical protein unknown function

Transposon Tn10 Accession # AY528506
Nucleotide Accession # NC_000913
Protein Accession # NP_415540

NACGACCGGATCCGG
GATCATATGACAAGATGTGTATCCACCTTAACTTAATGATTTTTACCAAAATCATTAGGGGATTCATCAG
GGCCAGAAGCCGACTTCAGTTCTATTTTTTGCTGGCAGTGGCGAATGCCGTCGTGTTAATTGTCTGGGCGCT
GTACAATAAGCTGCGTTTTCAAAAACAGCAGCATCATGCAGCCTACCAATATACGCCGCAAGAATATGCAG
AGAGCTTAGCAATACCTGATGAGCTCTATCAGCAACTACAAAAAAGCCACAGGATGAGCGTACACTTCACC
AGCCAGGGGCAAATAAAAATGGTTGTTTCAGAAAAAGCGCTAGTCCGGGCATAAACACCCAAAACAAAGC
CCGGTTCGCCCGGGCTCTGCACCGATAACACACTTAACTGTAGGCATGCAGCGTACGTTGGCAAAGTGCCG
AACGTACGCANT

Figure 5-117

150G7-2 (4X)
prfC gene- Factor; protein translation and modification; peptide chain release factor RF-3.

Transposon Tn10 Accession # AY528506
Nucleotide Accession # AE000508
Protein Accession # AAC77328

ANACNCGTCCGG
GATCATATGACAAGATGTGTATCCACCTTAACTTAATGATTTTTACCAAAATCATTANGGGATTCATCAG
TGTGGTGTCCGGTAAATATGAAAAAGGCATNAAACTGCNCCACGAGCCCACTGCNAANGATGNGG
NAATCTCCGCCCCGCNGCCTCTCTGGCNGGTNNCCGTTCTCACCTTNNACACCNCCCCNNGCTCNC
NTNCNCTCCCNNACNNCNNNTTCTCTCNGCANCCCACTTNATCTNCCNNCNCCCTCCCNACGNNTC
CCNCCCCNCNGNNCNANTGNNTTGGCTNNCGNCCNNNANNCNCNCTCNTCCTGGCCTCNCTCNTT
ACNCNN

Figure 5-118

155F4-4 (20X)
ycdR gene (complement) - orf, unknown, product homologous to IcaB in S. aureus

Transposon Tn10 Accession # AY528506
Nucleotide Accession # AE000204
Protein Accession # AAC74108

NNCGATCCGG
GATCATTGACAAGATGTGTATCCACCTTAACTTAATGATTTTTACCAAAATCATTAGGGGATTCATCAG
CACTTGTTGCCACGTGGCAAAATATTCTCGATCGACCAACTCATCGCCAAATTTTACTTGTTTATCC
GCTGGCATATCNNCCCNNNNCGTACTAGTCGACGCGTGGCCANN

Figure 5-119

160A8-6 (20X)
yjjQ gene – putative regulator; not classified

Transposon Tn10 Accession # AY528506
Nucleotide Accession # AE000507
Protein Accession # AAC77321

CGNCCGGATCCGG
GATCATATGACAAGATGTGTATCCACCTTAACTTAATGATTTTTACCAAAATCATTAGGGGATTCATCAG
GGCATCAACCAGATAGCTTCATTGCTTAAGAAAAGTAATAAAACTATCAGCGCCCAAAAAAACAG
TGCGATGCGTCGACTGGCAATTCACAGCAACGCTGAAATGTATGCATGGATAAATAGCGCGCAGG
GTGCAAGAGAACTTAACTTGCCTTCTGTTTATGGAGATGCCGCAGAATGGAACACAGCCGAATTA
AGAAGAGAAATGTCGCACTCATAGAAAAATGCGTCATGAGTAGTATCGGTATTGAGAGTTTATTC
AGAAAGTTTGCGGGTAACCCTTATAAGCTCCATACCTATACCAGTCAGGAGTCATTTCAGGATGCC
ATGTCGCGGATATCCCNNCNCCNCGTACTAGTCGACGCGTGGCCAA

Figure 5-120

169G4-6 (18X)
ycdR gene (complement) - orf, unknown, product homologous to IcaB in S. aureus

Transposon Tn10 Accession # AY528506
Nucleotide Accession # AE000204
Protein Accession # AAC74108

AAAANCNCGCCGGACATCCCGGATCCGGGATCAT
ATGACAAGGATGTGTATCCACCTTAACTTAATGATTTTTACCAAAATCATTAGGGGATTCATCAG
TATTAATCGCCAATAATCCCTCATTAAAAGAGTTTGCCCAGCAAATTATTACCGTACAGGAAAAAT
CACCACAACGGATAATGCATATCNCNCNNNNNNGTACTAGTCGACGCGTGGCCACANAN